



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 104187

To: Terra Gibbs
Location: CM1-11E12
Art Unit: 1635
Tuesday, September 23, 2003

Case Serial Number: 09/840704

From: Beverly Shears
Location: Biotech-Chem Library
CM1-1E05
Phone: 308-4994

beverly.shears@uspto.gov

Search Notes

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SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
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Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

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Date completed: 09-23-03
Searcher: Beverly C 4999
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Number of Databases: 1

Search Site

_____ STIC
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Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
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Vendors

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_____ APS
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STIC-Biotech/ChemLib

104187

From: Gibbs, Terra
Sent: Wednesday, September 17, 2003 6:11 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search request...

RECEIVED

SEP 22 2003

Please search SEQ ID NO:1 of USSN 09/840,704.

TECH/LEGAL DIVISION
10/10/03

Please do a search in all commercial databases.

Terra Cotta Gibbs, Ph.D.
Art Unit 1635
CM1, 12A12
703-306-3221

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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Best Local Similarity 100.0%; Pred. No. 0;					
Matches 1789; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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DB	1	GAATTCATCTGTGCACTGCTACCGGAGTTCCCGGAGAGAGATCTCTGAGCCCGAGT	60		
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DB	121	TCCCAATCCAGGGACTCGCGCGCGGACGCTGCTATGGACGACATTTTCACTCAGTGC	180		
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DB	361	ACCCCTTGCATCTGGCAGCAGTCACTGACACCGTGATATGTACAGAGCTATTGAC	420		
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DB	421	TACAGGAGACATCAATGCACTGAATGAACACGGGAATGTGCCCTGCATATGCCCTGT	480		
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DB	481	TTTTGGGCGCAAGATCAAGTGGCAGAGACCTGTGGCAATGGGGCCCTTGTTCAGCATC	540		
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DB	541	TGTAACAGTATGGAGATGCTGTGACAAAGCCAGGACCCCTGAGAGAGCTTCTC	600		
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DB	601	CGAGAGCGGCGAGAGAGATGGGCGCAGAAATCTCAACCGTATTTCCATACAAGGACACATTC	660		
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AR182654
LOCUS
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

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Sequence 1 from patent US 6338958.
AR182654.1 GI:20225861
Unknown.
Unclassified.
1 (bases 1 to 1789)
Dedhar, S. and Hannigan, G.
Integrin-linked kinase and its uses
Patent: US 6338958-A 1 15-JAN-2002;
Location/Qualifiers
1. .1789

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BASE COUNT 443 a 489 c 480 g 377 t
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1789; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1741 CCGCTGTCAATTAAGTTTATGAAAAA 1789

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LOCUS Sequence 1 from patent US 6369205.
DEFINITION AR205732
ACCESSION AR205732
VERSION AR205732.1 GI:21503389
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1789)
AUTHORS Dedhar, S. and Hannigan, G.
TITLE Integrin-linked kinase and its uses
JOURNAL Patent: US 6369205-A 1 09-APR-2002;
FEATURES Location/Qualifiers
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Best Local Similarity	100.0%; Pred. No. 0;			
Matches 1789; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
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Qy	61	CCCGAGGATAAAGCTTTGGGGTTTCATCTCTCCCTGATCACTCCACAGTCTCCAGGCT	120	
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Db	961	ACACATGGATGCGGTATGGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1020	
Qy	1021	GTGACACAGAGCAGGCTGTGAAGTTTCTTTGGACATGCGAAGGGGATGGCTTCTCTA	1080	
Db	1021	GTGACACAGAGCAGGCTGTGAAGTTTCTTTGGACATGCGAAGGGGATGGCTTCTCTA	1080	
Qy	1081	CACACATAGAGCCCTCATCCACGACATGCACTCAATAGCCGTAGTGTAAATGATGAT	1140	
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Qy	1141	GAGGACATGATGCTCCGAAATTTAGCATGCTGATGCTCAAGTTCTTTTCCAATGCTCTGT	1200	
Db	1141	GAGGACATGATGCTCCGAAATTTAGCATGCTGATGCTCAAGTTCTTTTCCAATGCTCTGT	1200	
Qy	1201	CGCATGATGACACCTGCTGGGTAGCCCGGAGCTCTGAGAGAGAGCCCTGAAGACACA	1260	
Db	1201	CGCATGATGACACCTGCTGGGTAGCCCGGAGCTCTGAGAGAGAGCCCTGAAGACACA	1260	
Qy	1261	AACAGAGCTCAGCAGACATGTTGGAGTTTTCAGTGTCTTGTGGGAACCTGGTCACACGG	1320	
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Qy	1321	GAGTACCTTTGCTGACCTTCCCAATATGAGAGATTGGAATGAAGTGGCATTCGAAGGC	1380	
Db	1321	GAGTACCTTTGCTGACCTTCCCAATATGAGAGATTGGAATGAAGTGGCATTCGAAGGC	1380	
Qy	1381	CTTCGGGCTACCATCCACAGGATTTTCCCTCATGTTGTAAAGCTCATGAAGATCTGC	1440	
Db	1381	CTTCGGGCTACCATCCACAGGATTTTCCCTCATGTTGTAAAGCTCATGAAGATCTGC	1440	
Qy	1441	ATGAATGAAGACCTCTGCAAGCGACCAAAATTTTCACATGATTGTGCTTATCCTTTGAGAG	1500	
Db	1441	ATGAATGAAGACCTCTGCAAGCGACCAAAATTTTCACATGATTGTGCTTATCCTTTGAGAG	1500	
Qy	1501	ATGAGGACAAAGTAGGACTGGAAGTCTTGCCTGAACTCCAGAGGTGTGGGACATGGT	1560	
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Qy	1681	GGCGGCTCAGAGCTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1740	
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DEFINITION	Sequence 3 from patent US 6177273	DNA	linear	PAT 16-MAY-2001	
ACCESSION	AR125502	Sequence 3 from patent US 6177273	DNA	linear	PAT 16-MAY-2001
VERSION	AR125502.1	GI:14111564	DNA	linear	PAT 16-MAY-2001
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1789)				
AUTHORS	Bennett, C. Frank, and Cowser, L. M.				
TITLE	Antisense modulation of integrin-linked kinase expression				
JOURNAL	Patent: US 6177273-A 3 23-JAN-2001;				
FEATURES	Location/Qualifiers				
source	1. 1789				
BASE COUNT	443 a	488 c	480 g	378 t	

ORIGIN

Query Match 99.9%; Score 1787.4; DB 6; Length 1789;
 Best Local Similarity 99.9%; Pred. No. 0;
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 REFERENCE
 1 (bases 1 to 1789)
 Hannigan, G.E., Leung-Hogsteijn, C., Fitz-Gibbon, L., Coppolino, M.G.,
 Radeva, G., Filmus, D., Bell, J.C. and Dedhar, S.
 Regulation of cell adhesion and anchorage-dependent growth by a new
 beta 1-integrin-linked protein kinase
 Nature 379 (6560), 91-96 (1996)
 JOURNAL MEDLINE
 PUBMED 8538749

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REFERENCE 2 (bases 1 to 1789)
AUTHORS Dedhar, S. and Hannigan, G.E.
TITLE Direct Submission
JOURNAL Submitted (07-NOV-1995) Shoukat Dedhar, Cancer Biology Research,
Sunnybrook Health Science Centre and University of Toronto, 2075
Bayview Avenue, North York, Ont. M4N 3M5, Canada
REFERENCE 3 (bases 1 to 1789)
AUTHORS Dedhar, S. and Hannigan, G.E.
JOURNAL Submitted (21-MAY-1998) Shoukat Dedhar, Cancer Biology Research,
Sunnybrook Health Science Centre and University of Toronto, 2075
Bayview Avenue, North York, Ont. M4N 3M5, Canada
REMARK Sequence update by submitter
COMMENT On May 21, 1998 this sequence version replaced gi:2648173.
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ACCESSION	AX524966		
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ORGANISM	Homo sapiens (human)		
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REFERENCE			
AUTHORS	1 Specht, T., Hinzmann, B., Schmitz, A., Pilarsky, C., Dahl, E. and Rosenthal, A.		
TITLE	Human nucleic acid sequences derived from breast tumor tissue		
JOURNAL	Patent: EP 1236799-A 13 04-SEP-2002;		
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ACCESSION BD134433.1 GI:23229378
VERSION JP 200206643-A/11.
KEYWORDS Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1780)
AUTHORS Speft,T., Hintzman,B., Armin,S., Pitarski,C., Edgar,D. and Rosenthal,A.
TITLE Human nucleic acid sequence originating in mammary tumor tissue
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PF 19-MAR-1999 JP 2000536852
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PI DUHL EDGAR.
PI ANDRE ROSENTHAL
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Db 494 CAGAGGACCTGGTGGCAAAATGGGGCCCTTGTGACATCTGTAAACAAGTATGAGAGATGC 553
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Db 554 CTGTGGACAAAGCAAGCACCCCTGAGAGAGCTTCTCCGAGAGGGGCGAGAGATGG 613
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Db 614 GCCAGATCTCAACCGTATTCATACAGGACATTTCTGGAAGGGGACACCCGCACTC 673
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Db 674 GGCCCCGAAATGGAACCCCTGAAACAAACACTCTGCAATTGACTTCAAAACAGCTTAACCTCC 733
QY 743 TGACGAAGCTCAACGAGAATCACTCTGAGAGCTATGGAAGGGCGCTGGCAGGGCAATG 802
Db 734 TGACGAAGCTCAACGAGAATCACTCTGAGAGCTATGGAAGGGCGCTGGCAGGGCAATG 793
QY 803 ACATTGCTGAAGGTGCTGAAGGTTCGAGACTGGAGTACGAAGGAGGAGGACCTTCA 862
Db 794 ACATTGCTGAAGGTGCTGAAGGTTCGAGACTGGAGTACGAAGGAGGAGGACCTTCA 853
QY 863 ATGAAGAGTGTCCCGGCTCAGAGTATTTCTCGCATCAAAATGTGCTCCAGTGTAGGTG 922
Db 854 ATGAAGAGTGTCCCGGCTCAGAGTATTTCTCGCATCCAAATGTGCTCCAGTGTAGGTG 913
QY 923 CCTGCCAGTCTCCACCTGCTCTCATCTCTCATCACACATGGAATGCCGTATGGAT 982
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QY 983 CCCTCTACATGTACTACATGAAGGCCACCAATTTGTCGTGGACACAGAGCCAGGCTGTGA 1042
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QY 1043 AGTTTGTCTTGGACATGGCAAGGGGCATGGGCTTCTCCTACACACATAGAGCCCTCATCC 1102

RESULT 10	LOCUS BC001554	DEFINITION Homo sapiens integrin-linked kinase, mRNA (CDNA clone MGC:5051 IMAGE:3457801), complete cds.	1731 bp	mRNA	linear	PRI 06-JUN-2003
ACCESSION	BC001554					
VERSION	BC001554.1					
KEYWORDS	MGC.	GI:16306740				
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
AUTHORS	1 (bases 1 to 1731)					
	Strauberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klusner,R.D., Collins,F.S., Wagner,L., Shemen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Butow,K.H., Schaefer,C.F., Bat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Datchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schaefer,T.E., Brownstein,M.J., Uedin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.U., Bosak,S.A., McPwan,P.J.,					

TITLE	Morkern,K.J., Malek,J.A.,Gunnathre,P.H.,Richards,S., Morley,K.C., Hale,S., Garcia,A.M., Gay L.J., Hulik,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.U., Lu,X., Gibbs,R.A., Fahney,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Boiffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E., Schererch,A., Schein,J.E., Jones,S.O. and Marra,M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences <i>Proc. Natl. Acad. Sci. U.S.A.</i> 99 (26), 16899-16903 (2002)
JOURNAL	22388257
MEDLINE	12477932
REFERENCE	2 (bases 1 to 1731)
AUTHORS	Strausberg,R.
TITLE	Direct Submission
JOURNAL	Submitted (21-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: gcgabs-room@nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: The I.M.A.G.E. Consortium (LNL) Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www.sbcg.stanford.edu Contact: (Dickson, Mark) mcd@pxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAC Plate: 4 Row: a Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4758605.
Location/Qualifiers

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CDS	452 a	464 c	458 g	357 t
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BASE COUNT 452 a 464 c 458 g 357 t
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 Query Match 92.4%; Score 1652.6; DB 9; Length 1731.

Best Local Similarity 99.6%; Pred. No. 0;
Matches 1678; Conservative 0; Mismatch

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Qy	168	TTTCACTCAGTCCGGGAGGCGCAACG	AGTCGCGTTTCGCTGTGGCTGACAAACACGGA	227
Db	80	TTTCACTCAGTCCGGGAGGCGCAACG	AGTCGCGTTTCGCTGTGGCTGACAAACACGGA	139
Qy	228	GAACGACCTCAAC	CAGGGGACGATCATGTGCTTCTCCCCCTTGCAC	287
Db	140	GAACGACCTCAAC	CAGGGGACGATCATGTGCTTCTCCCCCTTGCAC	199
Qy	288	GGGCGGCTCTGCTGTGGTTGAGATG	TTTGATCATCGGGGGGCGGATCAATGTAATGAA	347
Db	200	GGGCGGCTCTGCTGTGGTTGAGATG	TTTGATCATCGGGGGGCGGATCAATGTAATGAA	259
Qy	348	CCGTGGGGATGACAC	CCCCCTGCATCTGGCAGCCAGTCATGGCACCCGTCATATTGTACA	407
Db	260	CCGTGGGGATGACAC	CCCCCTGCATCTGGCAGCCAGTCATGGCACCCGTCATATTGTACA	319
Qy	408	GAAGCTATTTCAGTAC	AAGGCAGATCAATGCGATGAATGAACACGGGAATGTGCCCT	467
Db	320	GAAGCTATTTCAGTAC	AAGGCAGATCAATGCGATGAATGAACACGGGAATGTGCCCT	379
Qy	468	GCATATGCTGTTTTT	TGGGCGCAGATCAAGTGGCAGAGGACCTGGTGCAATGGGCG	527
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Qy	528	CTTTGTCAGCATCTGTAAC	AAAGTATGAGAGATGCCTGTGGACAAAGCCCAAGGCACCCCT	587
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Qy	828	TCGAGACTGAGATCA	AGGAAGACGAGGACTTCAATGAAGATGTCTCCGGCTCAGGAT	887
Db	740	TCGAGACTGAGATCA	AGGAAGACGAGGACTTCAATGAAGATGTCTCCGGCTCAGGAT	799
Qy	888	TTTTCTCGCATCCAA	TGCTGCCAGTGCTCCAGTGCTAGGTGCTGCCAGTCTCCACTGCTCTCTCA	947
Db	800	TTTTCTCGCATCCAA	TGCTGCCAGTGCTCCAGTGCTAGGTGCTGCCAGTCTCCACTGCTCTCTCA	859
Qy	948	TCCTACTCTCATCA	CACACTGGATGGCGTATGGATCCCTCTACAATGTACTACATGAAGG	1007
Db	860	TCCTACTCTCATCA	CACACTGGATGGCGTATGGATCCCTCTACAATGTACTACATGAAGG	919
Qy	1008	CACCAATTTTCTG	TGACACAGCCAGGCTGTGAAGTTTTCCTTTTGACATGCCAAGGGG	1067
Db	920	CACCAATTTTCTG	TGACACAGCCAGGCTGTGAAGTTTTCCTTTTGACATGCCAAGGGG	979
Qy	1068	CATGGGCTTCTCTA	CACACACTAGAGCCCTCATCCACAGCATGCACTCAATAGCCGTAG	1127
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Qy	1128	TGTAATGATTTGAT	GAGACATGACTGCCCGAAATPAGCATGGCTGATGCTCAAGTTCTCTTT	1187

Db	1040	TGTAATGATTGATGAGGACATGACTGCCGGAATTAGCATGGCTGATGTCGAAGTTCTCTTT	1099
Qy	1188	CCAATGTCCTGGTCGCATGATGACACCTGCTGGGTAGCCCCGGAAGCTCTGCAGAAGAA	1247
Db	1100	CCAATGTCCTGGTCGCATGATGACACCTGCTGGGTAGCCCCGGAAGCTCTGCAGAAGAA	1159
Qy	1248	GCCTGAAGACACAAACAGACAGCTCAGCAGACATGTGGAGTTTTCAGTGCCTTCTGTGGGA	1307
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Qy	1308	ACTGGTGACACGGGAGGTACCTTTGTGACCTCTCCAAATATGGAGATTGGAAATGAAGGT	1367
Db	1220	ACTGGTGACACGGGAGGTACCTTTGTGACCTCTCCAAATATGGAGATTGGAAATGAAGGT	1279
Qy	1368	GGCATTGGAAAGGCTTCGGCCTACCATCCACAGGTATTTCCCTCATGTGTGTAAGCT	1427
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Qy	1428	CATGAAGATCTGCATGAATGAAGACCTGCAAGCGACCCAAATTTGACATGATTGTGCC	1487
Db	1340	CATGAAGATCTGCATGAATGAAGACCTGCAAGCGACCCAAATTTGACATGATTGTGCC	1399
Qy	1488	TATCCTTTGAAGAGATCAGGACAAGTAGGACTTGGAAAGTTCCTTGCTGAACTCCAGAGGT	1547
Db	1400	TATCCTTTGAAGAGATCAGGACAAGTAGGACTTGGAAAGTTCCTTGCTGAACTCCAGAGGT	1459
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Qy	1667	CTGTG--CGCAAGAGGGGCGGCTCAGAGCTTTGTTCATTGCGCACATGGTGTCTCCCAAC	1724
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Qy	1725	ATGGGAGGATCAGCCCCCTGTCACATAAAGTTTATTATGAATAAATAAATAAATAA	1784
Db	1640	ATGGGAGGATCAGCCCCCTGTCACATAAAGTTTATTATGAATAAATAAATAAATAA	1699
Qy	1785	AAAAA 1789	
Db	1700	AAAAA 1704	

RESULT 11	
MMU94479	
LOCUS	1750 bp mRNA linear ROD 02-JAN-1998
DEFINITION	Mus musculus integrin binding protein kinase mRNA, complete cds.
ACCESSION	U94479
VERSION	U94479.1 GI:2739449
KEYWORDS	.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	Li, F., Liu, J., Mayne, R. and Wu, C.
TITLE	Identification and characterization of a mouse protein kinase that is highly homologous to human integrin-linked kinase
JOURNAL	Biochim. Biophys. Acta 1358 (3), 215-220 (1997)
MEDLINE	98031580
PUBMED	9366252
REFERENCE	2 (bases 1 to 1750)
AUTHORS	Wu, C. and Li, F.
TITLE	Direct Submission
JOURNAL	Submitted (18-MAR-1997) Cell Biology, University of Alabama at Birmingham, 1670 University Blvd., 217 Volker Hall, Birmingham, AL 35294-0019, USA
FEATURES	Location/Qualifiers
source	1..1750

RESULT 13	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE
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		Cavia porcellus beta-integrin-linked kinase mRNA, complete cds.				
		AF256520				
		AF256520.1	GI:7862154			
		Cavia porcellus (domestic guinea pig)				

ORGANISM	Cavia porcellus
Eukaryote:	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia:	Eutelia; Rodentia; Hystricognathi; Caviidae; Cavia.
REFERENCE	1 (bases 1 to 1693)
AUTHORS	Ishii,T., Satoh,E. and Nishimura,M.
TITLE	Integrin-linked kinase controls neurite outgrowth in NIE-115 neuroblastoma cells
JOURNAL	J. Biol. Chem. 276 (46), 42994-43003 (2001)
MEDLINE	21560993
PUBMED	11560928
REFERENCE	2 (bases 1 to 1693)
AUTHORS	Ishii,T.
TITLE	Direct Submision
JOURNAL	Submitted (15-APR-2000) Veterinary Pharmacology, University of Obihiro, School of Veterinary Medicine, Nishi 2-sen 11, Inada-Chou, Obihiro, Hokkaido 080-8555, Japan
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ORIGIN	K "
Query Match	77.3%; Score 1382.2; DB 10; Length 1693;
Best Local Similarity	90.6%; Pred. No. 0;
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Oy	407 AGAAGCATTTGACGTAACAAGGACAGACATCAATGACGTGAATGAACAACGGGAATGTGCCCC 466
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QY 1487 CTATCTTTGAGAAGATGACAGACAGTAGGACTTGAAGTCTTGGCTGAA-CTCCAGAG 1545
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RESULT 14

AC132877

LOCUS

DEFINITION

Mus musculus clone RP24-216J21, WORKING DRAFT SEQUENCE, 7 unordered

pieces.

AC132877

AC132877.3 GI:28927732

HTG; HTGS_PHASE1; HTGS_DRAFT.

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi;

Birren,B., Nusbaum,C. and Lander,E.

1 (bases 1 to 192539)

Mus musculus, clone RP24-216J21

Unpublished

REFERENCE

2 (bases 1 to 192539)

AUTHORS

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,

Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,

Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,

Cook,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S.,

Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,

Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,

Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,

Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,

Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,

McCarthy,M., Meldrum,J., Meneus,L., Mihova,T., Mienga,V.,

Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,

O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,

Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,

Roman,J., Roy,A., Schauer,S., Schuback,R., Seaman,S., Severy,P.,

Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,

Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,

Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,

Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

TITLE

JOURNAL

Submitted (04-SEP-2002) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE

3 (bases 1 to 192539)

AUTHORS

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,

Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,

Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,

Cook,A., Cooke,P., Corum,B., DeArelano,K., Faro,S.,

Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Fero,S.,

Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,

Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,

Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,

Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,

Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C.,

Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,

Meldrum,J., Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J.,

Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,

O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,

Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,

Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C.,

Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,

Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,

Vassiliev,H., Venkataram,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,

Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE
JOURNAL
COMMENT

Direct Submission
Submitted (12-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 12, 2003 this sequence version replaced g1:28412043.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: W1BR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L27122

Center clone name: 216-J 21

Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.96071

Consensus quality: 19104 bases at least Q40

Consensus quality: 191385 bases at least Q30

Insert size: 191939; sum-of-contigs

Quality coverage: 9.6 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 7935: contig of 7935 bp in length
* 7936 8035: gap of 100 bp
* 8036 10717: contig of 2682 bp in length
* 10718 10817: gap of 100 bp
* 10818 21133: contig of 10316 bp in length
* 21134 21233: gap of 100 bp
* 21234 37038: contig of 15805 bp in length
* 37039 37138: gap of 100 bp
* 37139 73158: contig of 36020 bp in length
* 73159 73258: gap of 100 bp
* 73259 134748: contig of 61490 bp in length
* 134749 134848: gap of 100 bp
* 134849 192539: contig of 57691 bp in length.

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Best Local Similarity 86.2%; Pred. No. 0; Indels 22; Gaps 6;
Matches 1452; Conservative 0; Mismatches 211

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DB	100401	CAACAGTTTCACTAGTCCCGGAGGCGACGAGCTCCGCTTGGCTGTGACAA	100455
QY	222	CACGAGAGACGCTCCAGGAGGAGATGAGCTTCCCTTGGCACTGGGCGCTG	281
DB	100456	CACGAGAGATGAGCTCCAGGAGGAGATGAGCTTCCCTTGGCACTGGGCGCTG	100515
QY	282	CCGAGAGGCGGCTTCTGCTGTTGAGATGTTGATCATGCGGGGCGACGAGTCAATGT	341
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QY	642	TCCATACAGAGCACTTCTGAAAGGAGGACCCGCTCGGCGCCGCAATGGAACCT	701
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 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 209228)
 Birren,B., Nusbaum,C. and Lander,E.
 Mus musculus, clone RP23-61L24
 Unpublished
 2 (bases 1 to 209228)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fato,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,

TITLE JOURNAL REFERENCE AUTHORS

Submitted (26-AUG-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 209228)

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fato,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kellis,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C., McCarthy,M., Meldrim,J., Menus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE JOURNAL COMMENT

Submitted (20-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Aug 20, 2002 this sequence version replaced gi:15290930.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information

Center project name: L14395

Center clone name: 61_L24

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 208109 bases at least Q40

Consensus quality: 208763 bases at least Q30

Consensus quality: 208883 bases at least Q20

Insert size: 220000; agarose-fp

Insert size: 208928; sum-of-ctngs

Quality coverage: 14.5 in Q20 bases; agarose-fp

Quality coverage: 15.3 in Q20 bases; sum-of-ctngs

* NOTE: This is a 'working draft' sequence. It currently

* consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 13553: contig of 13553 bp in length

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Dd	174048	TAACTCATGAAAGATTTGCAATGAAAGACCTTGCMAATTCACCCAAATTTGACATGAT	174107
Qy	1482	TGTGCTTATCTTGAAGATGACAGACAAATGAGACTGGAAGTCTTGGCTGAACTCC	1541
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Dd	174228	CTCCCGTGTCTTATCATGTGATTAACCCCAATGTAGGGGGCTGTGTTCCCTGCATC	174287
Qy	1662	CTACCACTGT---GGCGAAAGAGGGCGGGCTCAGAGCTTTGCACTTGGCACAATGCTGC	1717
Dd	174288	CTACCACTGTAGCCCCAAAGGGCTGGGGCTTGAAGCTTTGTCACCTTGGCACAATGCTGC	174347
Qy	1718	TCCCAACATGGGAGGATCAGCCCGCTGTGTCAATTAAGTTTATGAAAAAAGAAAA	1777
Dd	174348	TCCCAACATGGGAGGATCAGCCCGCTGTGTCAATTAAGTTTATGAAAAAAGAAAA	174407
Qy	1778	AAAAA 1782	

Db 174408 GAAGA 174412

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 22, 2003, 15:19:24 ; Search time 369 Seconds
(without alignments)
13087.519 Million cell updates/sec

Title: US-09-840-704a-1

Perfect score: 1789

Sequence: 1 gaattcattcgtcgcgtcct.....aaaaaaaaaaaaaaaaaaaa 1789

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*

4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*

6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*

7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*

8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*

9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*

10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*

11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*

12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*

13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*

14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*

15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*

16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*

17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*

18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*

19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*

20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*

22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*

23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*

24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1787.4	99.9	1789	22	AAf69274
2	1787.4	99.9	1789	24	ABK84315
3	1773	99.1	1786	18	AA771716
4	1771.4	99.0	1786	25	ACA56473
5	1693.4	94.7	1780	20	AA233623
6	1352.6	75.6	1607	21	AAf18117
7	1195.8	66.8	1359	22	AAf90197
8	466.8	26.1	1820	23	ABL15659

c	9	451.2	25.2	567	22	AAH09626
c	10	328.4	18.4	330	21	AA78148
c	11	328.4	18.4	330	22	AA128866
c	12	328.4	18.4	330	25	AB233072
c	13	305	17.0	4354	23	ABL16568
c	14	240.8	13.5	568	22	AAH35546
c	15	228.8	12.8	285	25	ABX74732
c	16	133.8	7.5	152	19	AAV33551
c	17	127.8	7.1	301	24	ABK62280
c	18	90.2	5.0	508	22	AAH04110
c	19	84.8	4.7	6843	25	ABX34513
c	20	84.8	4.7	7185	22	AAH57380
c	21	75.6	4.2	2355	24	ABA90356
c	22	75.6	4.2	2355	25	ABZ24424
c	23	75.6	4.2	3981	24	AB212023
c	24	75.4	4.2	896	22	AA332335
c	25	75.4	4.2	1640	24	ABN85315
c	26	75.4	4.2	1783	22	AA160004
c	27	75.4	4.2	2894	22	AA158218
c	28	75.4	4.2	4935	25	AAH51581
c	29	75	4.2	977	22	AA333358
c	30	73.4	4.1	696	20	AA335854
c	31	72.4	4.0	2499	22	AA506739
c	32	71.2	4.0	1288	21	AAZ49052
c	33	71.2	4.0	1345	21	AAZ94868
c	34	70.8	4.0	3876	22	AAH15762
c	35	67.6	3.8	3517	23	ABL10131
c	36	67	3.7	621	22	AAK52295
c	37	67	3.7	678	18	AA766424
c	38	67	3.7	780	20	AA35852
c	39	67	3.7	1468	18	AA766425
c	40	66.4	3.7	5482	22	AAf63955
c	41	66.4	3.7	5484	23	ABL08154
c	42	66.4	3.7	10194	23	ABL08154
c	43	65.4	3.7	696	20	AA35853
c	44	65.4	3.7	1534	25	AAH9614
c	45	64.8	3.6	3779	25	ABX34495

ALIGNMENTS

RESULT 1
ID AAF69274 standard; DNA, 1789 BP.
XX AAF69274;
AC AAF69274;
XX
XX 18-APR-2001 (first entry)
XX
XX Human integrin-linked kinase DNA.
DE Antisense; integrin-linked kinase; hIK; infection; tumour;
XX Inflammation; ds.
XX
XX Homo sapiens.
XX
XX US6177273-B1.
XX
XX 23-JAN-2001.
XX
XX 26-OCT-1999; 99US-0428219.
XX
XX 26-OCT-1999; 99US-0428219.
XX
XX 26-OCT-1999; 99US-0428219.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Cowsett LM;
XX WPI; 2001-137069/14.
XX
XX Novel antisense compounds capable of modulating expression of human
XX Integrin-linked kinase, useful for diagnosis, prophylaxis and treatment
PT

Human cDNA clone (cDNA encoding huma Colon tumour relat Human colon tumour Drosophila melanog Human colon cancer Human cDNA sequenc Clone 184416 cDNA Rat sequence diffe Human cDNA clone (Human mdct cDNA SE Human skeletal mus Human polynucleoti Human death associ Human polynucleoti DNA encoding human Human cytoskeleton Human polynucleoti Human polynucleoti Human structural a DNA encoding human DNA encoding rat g Polynucleotide seq Human ankyrin fami Human MHC class II Human cDNA sequenc Drosophila melanog Human polynucleoti Human P28 coding s DNA encoding human Drosophila tankyrs Drosophila melanog DNA encoding mouse Human cytoskeleton Human mdct cDNA SE

of diseases, e.g. tumors, associated with expression of the kinase -

Example 13; Column 47-50; 40pp; English.

The present invention relates to an antisense compound 8 to 30 bases in length targeted to the 5' untranslated (UTR) region, the coding region or the 3' UTR region human Integrin-linked kinase (hIK). The antisense oligonucleotides are useful for inhibiting the expression of human hIK in human cells or tissues, in vitro. The oligonucleotides can be utilized for diagnostics, therapeutics for the treatment of diseases associated with the expression of hIK, prophylaxis e.g. to prevent or delay infection, inflammation or tumor formation and as research reagent.

Sequence 1789 BP; 443 A; 488 C; 480 G; 378 T; 0 other;

Query Match 99.9%; Score 1787.4; DB 22; Length 1789;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAATTCATCTGCTGACTCTACCACGGAGCTCCCGGAGAGGATCTGCGAGCCCGAGT 60
Db 1 GAATTCATCTGCTGACTCTACCACGGAGTTCGCCGAGAGGATCTGCGAGCCCGAGT 60
QY 61 CCCGAGGATAAAGCTTGGGGTTCACTCTCTCCCTGGATCACTCCACAGTCCTCAGGCT 120
Db 61 CCCGAGGATAAAGCTTGGGGTTCACTCTCTCCCTGGATCACTCCACAGTCCTCAGGCT 120
QY 121 TCCCAATCCAGGGGACTCGCGCGGGACGCTGCTATGAGCAGCATTTTCACTCAGTGC 180
Db 121 TCCCAATCCAGGGGACTCGCGCGGGACGCTGCTATGAGCAGCATTTTCACTCAGTGC 180
QY 181 CGGAGGCAACGAGTCCGCTTCCCTTGGCTGGACACACGAGAACGACCTCAAC 240
Db 181 CGGAGGCAACGAGTCCGCTTCCCTTGGCTGGACACACGAGAACGACCTCAAC 240
QY 241 CAGGGGACGATCATGGCTTCTCCCTTGGCTGGGCTCGCGAGAGGGCGCTCTGCT 300
Db 241 CAGGGGACGATCATGGCTTCTCCCTTGGCTGGGCTCGCGAGAGGGCGCTCTGCT 300
QY 301 GTGTTGAGATGTTGATCATCGGGGGGACCGGATCAATGTAATGAACCGTGGGGATGAC 360
Db 301 GTGTTGAGATGTTGATCATCGGGGGGACCGGATCAATGTAATGAACCGTGGGGATGAC 360
QY 361 ACCCCCTGCATCTGGCAGCAGTCATGGACACCGTGTATTTGACAAAGCTATTGCGAG 420
Db 361 ACCCCCTGCATCTGGCAGCAGTCATGGACACCGTGTATTTGACAAAGCTATTGCGAG 420
QY 421 TACAAGGCAGACATCAATGTCAGTGAATGAACACCGGAAATGTGCCCTGCATATGCCCTGT 480
Db 421 TACAAGGCAGACATCAATGTCAGTGAATGAACACCGGAAATGTGCCCTGCATATGCCCTGT 480
QY 481 TTTTGGGGCCCAAGATCAAGTGGCAGAGACCTGTGGCAATGGGGCCCTTTGTGAGCATC 540
Db 481 TTTTGGGGCCCAAGATCAAGTGGCAGAGACCTGTGGCAATGGGGCCCTTTGTGAGCATC 540
QY 541 TGTAACAAGTATGGAGAGATCGCTGTGCAACCAAGCAAGGACCCCTGAGAGAGCTTCTC 600
Db 541 TGTAACAAGTATGGAGAGATCGCTGTGCAACCAAGCAAGGACCCCTGAGAGAGCTTCTC 600
QY 601 CGAGAGCGGGCAGAGAGATGGCGCAGAAATCTCAACCGTATTTCCATACAAGGACACATTC 660
Db 601 CGAGAGCGGGCAGAGAGATGGCGCAGAAATCTCAACCGTATTTCCATACAAGGACACATTC 660
QY 661 TGGAAAGGGGACACCCGACCTCGGCCCGAAATGGAACCTTGAAACAAACACTCTGGGCATT 720
Db 661 TGGAAAGGGGACACCCGACCTCGGCCCGAAATGGAACCTTGAAACAAACACTCTGGGCATT 720
QY 721 GACTTCAACAGCTTAACTCTTGACGAGCTCAACGAGATCACTCTGGAGAGCTATGG 780
Db 721 GACTTCAACAGCTTAACTCTTGACGAGCTCAACGAGATCACTCTGGAGAGCTATGG 780
QY 781 AAGGCCCGCTGGCAGGGCAATGACATTTGCTGGAAGGTGCTGAAGGTTCGAGAGCTGGAGT 840

RESULT 2
ABK84315
ID ABK84315 standard; cDNA; 1789 BP.
XX
AC ABK84315;

Seq	Sequence	1789 BP: 443 A; 488 C; 480 G; 378 T; 0 other;	Query Match	99.9%; Score 1787.4; DB 24; Length 1789;	Best Local Similarity	99.9%; Pred. No. 0;	Matches 1788; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1	GAATTCATCTGTGACATGCTACACACGGAGAGTCCCGGAGAGAGATCTCTGACGCCGAGT	60					
1	GAATTCATCTGTGACATGCTACACACGGAGAGTCCCGGAGAGAGATCTCTGACGCCGAGT	60					
61	CCCGAGATTAAGCTTGGGGTTCACTCTCTCCCTGGATCAGTCCACAGTCCAGGCT	120					
61	CCCGAGATTAAGCTTGGGGTTCACTCTCTCCCTGGATCAGTCCACAGTCCAGGCT	120					
121	TCGCCAATCCAGGGGACCTCGGCGCCGGGACGCTCTATGACGACATTTTCACTCAGTGC	180					
121	TCGCCAATCCAGGGGACCTCGGCGCCGGGACGCTCTATGACGACATTTTCACTCAGTGC	180					
181	CGGAGGGGCAACGGAGTGGCCGTTGCGCTGTGAGTGAACAACGAGAAAGCATCTCAAC	240					
181	CGGAGGGGCAACGGAGTGGCCGTTGCGCTGTGAGTGAACAACGAGAAAGCATCTCAAC	240					
241	CAGGGGGACGATCATGGCTTTCCCCCTTGCATCTGGGCTTCGCCAGAGGGCCGCTCGCT	300					
241	CAGGGGGACGATCATGGCTTTCCCCCTTGCATCTGGGCTTCGCCAGAGGGCCGCTCGCT	300					
301	GTGGTTGAGTGTGATCATGCTGGGGGGCAACGATCATGTAATGTAACCGTGGGGATGAC	360					
301	GTGGTTGAGTGTGATCATGCTGGGGGGCAACGATCATGTAATGTAACCGTGGGGATGAC	360					
361	ACCCCGCTGCATCTGGCAGCCAGTCATGACACCCGTGATATTGACAGAACTATTGACAG	420					
361	ACCCCGCTGCATCTGGCAGCCAGTCATGACACCCGTGATATTGACAGAACTATTGACAG	420					
421	TACAAAGCAGATCATATGACAGTGAATGAACACGGGAATGTGCCCTGCACTATGCTGT	480					
421	TACAAAGCAGATCATATGACAGTGAATGAACACGGGAATGTGCCCTGCACTATGCTGT	480					
481	TTTTGGGGGCCAAGATCAAGTGGCAGAGGACCTGGTGGCAAAATGGGGCCCTTGTGAGATC	540					
481	TTTTGGGGGCCAAGATCAAGTGGCAGAGGACCTGGTGGCAAAATGGGGCCCTTGTGAGATC	540					
541	TGTAAACAAGTATGAGAGAGATGCTGTGGGCAAAACCAAGGACCCCTGAGAGACTTCTC	600					
541	TGTAAACAAGTATGAGAGAGATGCTGTGGGCAAAACCAAGGACCCCTGAGAGACTTCTC	600					
601	CGAGAGCGGGCAGAGAGATGGGCGAGATCTCAACCGTATTCATACAGAGACATTC	660					
601	CGAGAGCGGGCAGAGAGATGGGCGAGATCTCAACCGTATTCATACAGAGACATTC	660					
661	TGGAAGGGGACACCCCGCACTGGGCCCCGGAATGGAACCCGGAACAAACCTCTGGCATT	720					
661	TGGAAGGGGACACCCCGCACTGGGCCCCGGAATGGAACCCGGAACAAACCTCTGGCATT	720					
721	GACTTCAACAAGCTTAACTTCTCTACAGAGCTCAACAGAAATCACTCTGGAGACTATGG	780					
721	GACTTCAACAAGCTTAACTTCTCTACAGAGCTCAACAGAAATCACTCTGGAGACTATGG	780					
781	AAGGGCCGCTGGCAGGGCAATGACATTGTCTGTAAGGTCTGAAGGTTGAGACTGAGT	840					
781	AAGGGCCGCTGGCAGGGCAATGACATTGTCTGTAAGGTCTGAAGGTTGAGACTGAGT	840					
841	ACAAGGAAGACACAGGACCTTAATGAAGAAGTCTCCCGGCTCAAGATTTTCTGCAATCA	900					
841	ACAAGGAAGACACAGGACCTTAATGAAGAAGTCTCCCGGCTCAAGATTTTCTGCAATCA	900					
901	AATGTCATCCAGTGTAGTGTCTGCGACAGTCTCACCTGCTCTCAATCTCACTCTATC	960					
901	AATGTCATCCAGTGTAGTGTCTGCGACAGTCTCACCTGCTCTCAATCTCACTCTATC	960					
961	ACACATCTGATGCGGTATGATCCCTCTTACATGTACTACATGAAGGACCAATTTTCTC	1020					

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Db 961 ACACACTGGATGCGGTATGGATCCCTCACAATGTACTACATGAAGGCACCAATTTTCGTC 1020
QY 1021 GTGACACAGAGCCAGGCTGTGAAGTTTCTTTGGACATGGCAGGGGATGGCTTCTCTA 1080
Db 1021 GTGACACAGAGCCAGGCTGTGAAGTTTCTTTGGACATGGCAGGGGATGGCTTCTCTA 1080
QY 1081 CACACACTAGAGCCCTCATCCCGACATGCACCTCAATAGCCGTAGTGTAAATGATTGAT 1140
Db 1081 CACACACTAGAGCCCTCATCCCGACATGCACCTCAATAGCCGTAGTGTAAATGATTGAT 1140
QY 1141 GAGGACATGACTGCCCCGAATTAGCATGCTGATGTCAAGTTTCTTTTCCAATGCTCGGT 1200
Db 1141 GAGGACATGACTGCCCCGAATTAGCATGCTGATGTCAAGTTTCTTTTCCAATGCTCGGT 1200
QY 1201 CGCATGTATGACCTGCTGGGTAGCCGCCGAGCTCTGCAGAGAAGCCCTGAAGACACA 1260
Db 1201 CGCATGTATGACCTGCTGGGTAGCCGCCGAGCTCTGCAGAGAAGCCCTGAAGACACA 1260
QY 1261 AACAGACCTCAGCAGACATGTGGAGTTTTCAGTGTCTTGTGGAACTGGTGACACGG 1320
Db 1261 AACAGACCTCAGCAGACATGTGGAGTTTTCAGTGTCTTGTGGAACTGGTGACACGG 1320
QY 1321 GAGGTACCTTTGTGACCTCTCCAATATGAGATTTGAATGAAAGTGGCATTTGAAGGC 1380
Db 1321 GAGGTACCTTTGTGACCTCTCCAATATGAGATTTGAATGAAAGTGGCATTTGAAGGC 1380
QY 1381 CTTGGGCTTACATCCACACAGGTATTTCCCTCATGTGTAGCTCATGAAGATCGC 1440
Db 1381 CTTGGGCTTACATCCACACAGGTATTTCCCTCATGTGTAGCTCATGAAGATCGC 1440
QY 1441 ATGAATGAAGACCTCTCAAGCGACCCCAATTTGACATGATTGTGCTTATCTTTGAGAAG 1500
Db 1441 ATGAATGAAGACCTCTCAAGCGACCCCAATTTGACATGATTGTGCTTATCTTTGAGAAG 1500
QY 1501 ATGCAGGACAAGTAGACTGGAAGTCTTGCCTGAACTCCAGAGGTGTGGGACATGGT 1560
Db 1501 ATGCAGGACAAGTAGACTGGAAGTCTTGCCTGAACTCCAGAGGTGTGGGACATGGT 1560
QY 1561 TGGGGGAATGACCTCTCCCAAGCAGCAGGCTCTGGTTGCTCCCGCCCTCCAGTCTAT 1620
Db 1561 TGGGGGAATGACCTCTCCCAAGCAGCAGGCTCTGGTTGCTCCCGCCCTCCAGTCTAT 1620
QY 1621 GGTACTACCCAGCCTGGGGTCCATPCCCTTCCCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 1680
Db 1621 GGTACTACCCAGCCTGGGGTCCATPCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 1680
QY 1681 GCGGGCTCAGAGCTTTGTCTCCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
Db 1681 GCGGGCTCAGAGCTTTGTCTCCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
QY 1741 CCGCTGTGCAATAAAGTTTATTATGAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1789
Db 1741 CCGCTGTGCAATAAAGTTTATTATGAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1789
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RESULT 3

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AA71716
ID AA71716 standard; cDNA; 1786 BP.
XX
AC AA71716;
XX
DT 29-SEP-1997 (first entry)
XX
DE Human integrin-linked kinase (ILK) cDNA.
XX
KW Integrin-linked kinase; ILK; serine/threonine kinase; cell growth;
KW cell adhesion; cell migration; cell invasion; inhibitor;
KW gene therapy; diagnosis; cancer; leukaemia; tumour; inflammation;
KW arthritis; osteoporosis; cardiovascular disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
SQ Sequence 1786 BP; 443 A; 487 C; 479 G; 377 T; 0 other;
Query Match 99.1%; Score 1773; DB 18; Length 1786;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 1 GAAATTCATCTCTGACCTGCTACACGAGGAGTTCCCGGAGAGGATCCTGCAGGCCGAGT 60
Db 1 GAAATTCATCTCTGACCTGCTACACGAGGAGTTCCCGGAGAGGATCCTGCAGGCCGAGT 60
QY 61 CCCGAGGATAAAGCTTGGGGTTTCATCTCTTCCCTCGATCCTCCACAGTCTCCAGGCT 120
Db 61 CCCGAGGATAAAGCTTGGGGTTTCATCTCTTCCCTCGATCCTCCACAGTCTCCAGGCT 120
QY 121 TCCCAATCCAGGGAGCTCGCGCGGGAGCTGCTATGGAGCAGATTTTCACTCAGTGC 180
Db 121 TCCCAATCCAGGGAGCTCGCGCGGGAGCTGCTATGGAGCAGATTTTCACTCAGTGC 180
QY 181 CGGAGGGCAACGACAGTCCGCTTCCGCTGTGGCTGGACAAACACGGAGAACGACCTCAAC 240
Db 181 CGGAGGGCAACGACAGTCCGCTTCCGCTGTGGCTGGACAAACACGGAGAACGACCTCAAC 240
QY 241 CAGGGGACGATCATGCTTCTCCCTTGCATCTGGGCTCCCGAGAGGGCGCTCTGCT 300
Db 241 CAGGGGACGATCATGCTTCTCCCTTGCATCTGGGCTCCCGAGAGGGCGCTCTGCT 300
QY 301 GTGGTTGAGATGTTGATCATGCGGGGCGACGGATCAATGTAATCAACCCGTGGGGATGAC 360
Db 301 GTGGTTGAGATGTTGATCATGCGGGGCGACGGATCAATGTAATCAACCCGTGGGGATGAC 360
QY 361 ACCCCCTGTCATCTGGCAGCCAGTATGGACACCGTGATATTGTACAGAAGCTATTGCGAG 420
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Db      361  ACCCCCTGCACTCTGGACGCCAGTCATGAGACCGTGATATTGTACAGAGCTATTGGAG 420
Qy      421  TACAAGGAGACATCAATGCACTGATGAATGAACACGGGAATGTGCCCCCTGCACTATCCCTGT 480
Db      421  TACAAGGAGACATCAATGCACTGATGAATGAACACGGGAATGTGCCCCCTGCACTATCCCTGT 480
Qy      481  TTTTGGGGCCCAAGATCAAGTGGCAGAGGACCTGGTGGGAAATGGGGCCCTTGTGCAGATC 540
Db      481  TTTTGGGGCCCAAGATCAAGTGGCAGAGGACCTGGTGGGAAATGGGGCCCTTGTGCAGATC 540
Qy      541  TGTAAACAATATGAGAGATGCTGTGAGCAAAAGCCAAAGGACCCCTGAGAGAGCTTCTC 600
Db      541  TGTAAACAATATGAGAGATGCTGTGAGCAAAAGCCAAAGGACCCCTGAGAGAGCTTCTC 600
Qy      601  CGAGAGCCGGGCGAGAGAAATGGGGCCAGATCTCAACCGTATTCTCATACAGAGACATTC 660
Db      601  CGAGAGCCGGGCGAGAGAAATGGGGCCAGATCTCAACCGTATTCTCATACAGAGACATTC 660
Qy      661  TGGAAAGGGGACACCCGCACTCGGCCCCGAAATGGAACCTGGAACAAACACTTGGCAAT 720
Db      661  TGGAAAGGGGACACCCGCACTCGGCCCCGAAATGGAACCTGGAACAAACACTTGGCAAT 720
Qy      721  GACTTCAAAACAGCTTAATCTTCTGACGAAGCTCAACGAGAACTCACTCTGAGAGCTATG 780
Db      721  GACTTCAAAACAGCTTAATCTTCTGACGAAGCTCAACGAGAACTCACTCTGAGAGCTATG 780
Qy      781  AAGGCCCCCTGGCGAGGCAATGACATTGTCTGTAAAGTGTCTGAGAGCTTGAGACTGAGT 840
Db      781  AAGGCCCCCTGGCGAGGCAATGACATTGTCTGTAAAGTGTCTGAGAGCTTGAGACTGAGT 840
Qy      841  ACAAGGAGAGAGGAGGACTTCAATGAAGTGTCCCCGGCTCAGAGATTTCTCGGATCCA 900
Db      841  ACAAGGAGAGAGGAGGACTTCAATGAAGTGTCCCCGGCTCAGAGATTTCTCGGATCCA 900
Qy      901  AATGTGCTCCAGTGTCTAGTGTGCTGCGCAGTCTCCACGCTCCTCATCTCTACTCTCATC 960
Db      901  AATGTGCTCCAGTGTCTAGTGTGCTGCGCAGTCTCCACGCTCCTCATCTCTACTCTCATC 960
Qy      961  ACACACTGGATGCCGTATGATCCCTCTTCAATGTAATGTAATGTAATGTAATGTAATG 1020
Db      961  ACACACTGGATGCCGTATGATCCCTCTTCAATGTAATGTAATGTAATGTAATGTAATG 1020
Qy      1021  GTGGACCAAGAGCCAGGCTGTGAAGTTTGTGTGACATGGAAGGGGCGATGGCTTCTCTA 1080
Db      1021  GTGGACCAAGAGCCAGGCTGTGAAGTTTGTGTGACATGGAAGGGGCGATGGCTTCTCTA 1080
Qy      1081  CACACACTAGAGCCCTCATCCACGACATGCACTCAATAGGCGTATGTAATGTAATGAT 1140
Db      1081  CACACACTAGAGCCCTCATCCACGACATGCACTCAATAGGCGTATGTAATGTAATGAT 1140
Qy      1141  GAGGACATGACTGCGCCGAATTAAGATGCTGATGTCGAAGTTCTCTTCCAAATGTCCTGT 1200
Db      1141  GAGGACATGACTGCGCCGAATTAAGATGCTGATGTCGAAGTTCTCTTCCAAATGTCCTGT 1200
Qy      1201  CGCATGTATGCACTGCTGGGTAGCCCCCGAAGCTCTGACAGAAAGCCTTAAAGACACA 1260
Db      1201  CGCATGTATGCACTGCTGGGTAGCCCCCGAAGCTCTGACAGAAAGCCTTAAAGACACA 1260
Qy      1261  AACAGACCTCTGAGAGATGAGATTTTGGAGTGTCTGTTGGGAACTGTTGACAGG 1320
Db      1261  AACAGACCTCTGAGAGATGAGATTTTGGAGTGTCTGTTGGGAACTGTTGACAGG 1320
Qy      1321  GAGTACCTCTTGTGCTGACCTCTCAATATGAGATTTGGAATGGAATGAGTGGCATTTGAGGC 1380
Db      1321  GAGTACCTCTTGTGCTGACCTCTCAATATGAGATTTGGAATGGAATGAGTGGCATTTGAGGC 1380
Qy      1381  CTTGGGCTTACATCCACAGGTAATTTCCCTCATGTGTGTAACCTCATGAAAGATCTGC 1440
Db      1381  CTTGGGCTTACATCCACAGGTAATTTCCCTCATGTGTGTAACCTCATGAAAGATCTGC 1440
Qy      1441  ATGAATGAAGACCTGCAAAAGGACCCAAATTTGACATGATGTGCTTATCTTGAAG 1500
Db      1441  ATGAATGAAGACCTGCAAAAGGACCCAAATTTGACATGATGTGCTTATCTTGAAG 1500

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Db      1438  ATGAATGAAGACCTGCAAAAGGACCCAAATTTGACATGATGTGCTTATCTTGAAG 1497
Qy      1501  ATGACAGGCAAGTGAAGTGAAGTCTTGTGCTGAATCCAGAGGTCTCGGAGATAGT 1560
Db      1498  ATGACAGGCAAGTGAAGTGAAGTCTTGTGCTGAATCCAGAGGTCTCGGAGATAGT 1557
Qy      1561  TGGGGGAATGCACTCCCAAGAGAGAGGCTCTGTGTGCTCCCGGCTCCAGTAT 1620
Db      1558  TGGGGGAATGCACTCCCAAGAGAGAGGCTCTGTGTGCTCCCGGCTCCAGTAT 1617
Qy      1621  GGTACTACCCAGCTGGGGTTCATCCCTTCCCATCTTCCATCTGTCGCAAGG 1680
Db      1618  GGTACTACCCAGCTGGGGTTCATCCCTTCCCATCTTCCATCTGTCGCAAGG 1677
Qy      1681  GCGGGGCTCAGAGCTTTGTCTTGTCCCATGTGTCTCCCAATGGAGGATCAGCC 1740
Db      1678  GCGGGGCTCAGAGCTTTGTCTTGTCCCATGTGTCTCCCAATGGAGGATCAGCC 1737
Qy      1741  CCGCTGTCACAATTAAGTTATTATGAAAAA 1789
Db      1738  CCGCTGTCACAATTAAGTTATTATGAAAAA 1786

RESULT 4
ACAS6473
ID ACAS6473 standard; cDNA; 1786 bp.
ACAS6473;
ACAS6473;
06-JUN-2003 (first entry)
Human signalling pathway polynucleotide probe SEQ ID NO 1071.
Human; probe; ss; array element; Parkinson's disease;
signalling pathway population; cancer; adenocarcinoma; leukemia;
immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
Homo sapiens.
US650938-B1.
31-DEC-2002.
30-JAN-1998; 98US-0016434.
30-JAN-1998; 98US-0016434.
(INCY-) INCYTE GENOMICS INC.
Au-Young J, Seilhamer J;
WPI; 2003-352189/33.
Combination of polynucleotide probes, useful as array elements in a
microarray for monitoring the expression of a number of target
polynucleotides -
Claim 1; SEQ ID NO 1071; 65bp; English.

The invention relates to a combination which, comprises a number of
polynucleotide probes comprising a sequence selected from one of the 1490
sequences mentioned in the specification. The combination is useful as an
array element in a microarray for monitoring the expression of a number
of target polynucleotides. The microarray is particularly useful in the
diagnosis and treatment of cancer and immunopathology and neuropathology.
The microarray is useful in diagnostics and treatment regimens, drug
discovery and development, toxicological and carcinogenicity studies,
forensics and pharmacogenomics. The microarray is also useful for
monitoring progression of diseases and for developing sophisticated
profiles for the effects of currently available therapeutic drugs. The
combination is also useful for purifying a subpopulation of mRNAs, cDNAs
and genomic fragments and in research and diagnostic applications. The
array can detect changes in expression in a large number of genes coding

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CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. ARDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention.

SQ Sequence 1786 BP; 443 A; 486 C; 479 G; 378 T; 0 other;

Query Match 99.0%; Score 1771.4; DB 25; Length 1786;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1785; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

Qy	1	GAATTCATCTCTCGACTCTCTACACCGGAGTTCCTCCGGAGAAAGGATCTCTGCAGCCCGAGT	60
Db	1	GAATTCATCTCTCGACTCTCTACACCGGAGTTCCTCCGGAGAAAGGATCTCTGCAGCCCGAGT	60
Qy	61	CCCAGAGATAAAGCTTGGGGTTTCATCTCTCTCCCTGGATCACTCCACAGTCCCTCAGGCT	120
Db	61	CCCAGAGATAAAGCTTGGGGTTTCATCTCTCTCCCTGGATCACTCCACAGTCCCTCAGGCT	120
Qy	121	TCCCAATTCAGGGGACTCGCGCCGGACGCTGCTATGGACGACATTTTCACTCAGTGC	180
Db	121	TCCCAATTCAGGGGACTCGCGCCGGACGCTGCTATGGACGACATTTTCACTCAGTGC	180
Qy	181	CGGAGGGCAACGCAGTCCGCGTTCCTGTGGCTGGACAACACGAGGAACGACCTCAAC	240
Db	181	CGGAGGGCAACGCAGTCCGCGTTCCTGTGGCTGGACAACACGAGGAACGACCTCAAC	240
Qy	241	CAGGGGACGATCATGGCTTCTCCCTTTGCACTGGGCTGCGAGAGGGCGCTCTGCT	300
Db	241	CAGGGGACGATCATGGCTTCTCCCTTTGCACTGGGCTGCGAGAGGGCGCTCTGCT	300
Qy	301	GTGTTTGAGATGTTTGAATCATCGGGGGGACGGATCAATGTAAATGAACCGTGGGATGAC	360
Db	301	GTGTTTGAGATGTTTGAATCATCGGGGGGACGGATCAATGTAAATGAACCGTGGGATGAC	360
Qy	361	ACCCCTTGATCTGGCAGCAGTCATGGACACCGTGATATTGTACAGAACTATTGGAG	420
Db	361	ACCCCTTGATCTGGCAGCAGTCATGGACACCGTGATATTGTACAGAACTATTGGAG	420
Qy	421	TACAAGGCAGACATCAATGTCAGTGAATGAACACGGGAATGCCCCCTGCACATATGCTGT	480
Db	421	TACAAGGCAGACATCAATGTCAGTGAATGAACACGGGAATGCCCCCTGCACATATGCTGT	480
Qy	481	TTTTTGGGCCAAGATCAAGTGGCAGAGGACCTGGTGGCAAAATGGGGCCCTTGTACGATC	540
Db	481	TTTTTGGGCCAAGATCAAGTGGCAGAGGACCTGGTGGCAAAATGGGGCCCTTGTACGATC	540
Qy	541	TGTAAACAGTATGGAGAGATGCTGTGGACAAGCAAGGCAACCCCTGAGAGAGCTTCTC	600
Db	541	TGTAAACAGTATGGAGAGATGCTGTGGACAAGCAAGGCAACCCCTGAGAGAGCTTCTC	600
Qy	601	CGAGCGGGCAGAGAAGATGGCCAGAACTCTCAACCGTATTCATACAAAGGACACATTC	660
Db	601	CGAGCGGGCAGAGAAGATGGCCAGAACTCTCAACCGTATTCATACAAAGGACACATTC	660
Qy	661	TGGAAGGGGACACCCGACCTCGGCCCGGAAATGGAACCCCTGAACAAAACACTCTGGCATT	720
Db	661	TGGAAGGGGACACCCGACCTCGGCCCGGAAATGGAACCCCTGAACAAAACACTCTGGCATT	720
Qy	721	GACTTCAACAGCTTTAACTTCTGTACGAACTCAACGAGAATCACTCTGGAGAGCTATGG	780
Db	721	GACTTCAACAGCTTTAACTTCTGTACGAACTCAACGAGAATCACTCTGGAGAGCTATGG	780
Qy	781	AAGGGCCGCTCGCAGGGCAATGACATTTGCTGGAAGGTGCTCAAGGTTTCGAGACTGGAGT	840
Db	781	AAGGGCCGCTCGCAGGGCAATGACATTTGCTGGAAGGTGCTCAAGGTTTCGAGACTGGAGT	840
Qy	841	ACAAGGAAGACAGGACTTCAATGAAGAGTGTCCCCCGCTCAGGATTTTCTCGCATCCA	900

841	ACAAGGAAGAGCAGGAGCTTCAATGAAGAGTGCCCGGGCTCAGAGATTTTCTCGCATCCA	900
901	AATGTGCTCCAGTGTAGTGTGCTGCCAGTCTCCACCTGCTCCTCATCTACTCTCATC	960
901	AATGTGCTCCAGTGTAGTGTGCTGCCAGTCTCCACCTGCTCCTCATCTACTCTCATC	960
961	ACACATGGAGTGCCTATGAGTCCCTCTACAAATGTAATAATGAAGCACCAATTTCTGCT	1020
961	ACACATGGAGTGCCTATGAGTCCCTCTACAAATGTAATAATGAAGCACCAATTTCTGCT	1020
1021	GTGGACACAGACCGAGCTGTGAAGTTTGTCTTGGACATGGCAAGGGGCGATGGGCTTCCCTA	1080
1021	GTGGACACAGACCGAGCTGTGAAGTTTGTCTTGGACATGGCAAGGGGCGATGGGCTTCCCTA	1080
1081	CACACACTAGAGCCCTCATCCACAGACATGCACTCAATAGCCGTAGTGTAAATGATTGAT	1140
1081	CACACACTAGAGCCCTCATCCACAGACATGCACTCAATAGCCGTAGTGTAAATGATTGAT	1140
1141	GAGGACATGACTGCCCGAATTAGCATGGCTGATGTCAAGTTCTCTTTTCCAAATGCTCTGGT	1200
1141	GAGGACATGACTGCCCGAATTAGCATGGCTGATGTCAAGTTCTCTTTTCCAAATGCTCTGGT	1200
1201	CGCATGTATGCACCTGCCCTGGGTAGCCCCCGAAGCTCTGCAGAGAAGAGCTGAAGACACA	1260
1201	CGCATGTATGCACCTGCCCTGGGTAGCCCCCGAAGCTCTGCAGAGAAGAGCTGAAGACACA	1260
1261	AACAGACGCTCAGCAGACATGTGGAGTTTGTGCACTGCTCTGTGGGAACTGGTGAACACGG	1320
1261	AACAGACGCTCAGCAGACATGTGGAGTTTGTGCACTGCTCTGTGGGAACTGGTGAACACGG	1320
1321	GAGGTACCTTTGCTGACCTCTCCAAATATGGAGATTGGAATGAAGTGGCATTGGAAGGC	1380
1321	GAGGTACCTTTGCTGACCTCTCCAAATATGGAGATTGGAATGAAGTGGCATTGGAAGGC	1380
1381	CTTTCGGCTTACCATCCACACAGGTATTTCCCTCATGTGTGTGAAGCTCATGAAGATCTGC	1440
1381	CTTTCG---TACCATTCCACACAGGTATTTCCCTCATGTGTGTGAAGCTCATGAAGATCTGC	1437
1441	ATGAATGAAGACCTGTCAAGCGCACCAAAATTTGACATGATCTGTGCTTCCCTTGAGAAG	1500
1438	ATGAATGAAGACCTGTCAAGCGCACCAAAATTTGACATGATCTGTGCTTCCCTTGAGAAG	1497
1501	ATGCAGGACAAGTAGGACTGGAAGAGTCTTTCCTGAACTCCAGAGGTGTGCGGACATGGT	1560
1498	ATGCAGGACAAGTAGGACTGGAAGAGTCTTTCCTGAACTCCAGAGGTGTGCGGACATGGT	1557
1561	TGGGGGAATGCACCTCCCAAGACAGAGGCCTCTGGTTGCTTCCCGGCTCCAGTCAAT	1620
1558	TGGGGGAATGCACCTCCCAAGACAGAGGCCTCTGGTTGCTTCCCGGCTCCAGTCAAT	1617
1621	GGTACTACCCACGCTGGGGTCCATCCCTTCCCATCCCTACCACTGTGCGCAAGAGG	1680
1618	GGTACTACCCACGCTGGGGTCCATCCCTTCCCATCCCTACCACTGTGCGCAAGAGG	1677
1681	GGCGGGCTCAGAGCTTTGTCACTTGCCACATGTGTCTCCCAACATGGGAGGATCAGCC	1740
1678	GGCGGGCTCAGAGCTTTGTCACTTGCCACATGTGTCTCCCAACATGGGAGGATCAGCC	1737
1741	CCGCTGTCAATAAAGTTTATTATGAAAAAATAAAAAAAAAAAAAA	1789
1738	CCGCTGTCAATAAAGTTTATTATGAAAAAATAAAAAAAAAAAAAA	1786

RESULT 5

RESUL 3
AAZ33623

AAZ33623
ID AAZ33623 standard; cDNA; 1780 BP.

2 XX

AC AAZ33623;

XX
XX

DT

Query Match	94.7%	Score 1693.4	DB 20	Length 1780
Best Local Similarity	99.1%	Pred. No. 0		
Matches 1745; Conservative	0	Mismatches	11	Indels 5; Gaps 4

Db	494	CAGAGACCTTGATGGCAAATGAGGGCCCTTGTGACGATCTGTACCACTATGTAGAGATGC	553
Qy	563	CTGTGACAAAGCCAAAGGCACTCCCTGAGAGAGCTTCTCGAGAGCGGGCAGAGAAATGG	622
Db	554	CTGTGACAAAGCCAAAGGCACTCCCTGAGAGAGCTTCTCGAGAGCGGGCAGAGAAATGG	613
Qy	623	GCCAGAACTCTAACCCGTAATTCATATCAAGGACATTTCTGGAAAGGGACCACTCCGCATCTC	682
Db	614	GCCAGAACTCTAACCCGTAATTCATATCAAGGACATTTCTGGAAAGGGACCACTCCGCATCTC	673
Qy	683	GGCCCCGAAATGGAACCTCGAACAACACCTCTGGCATTGACTTCAAAACAGTTAACTTCC	742
Db	674	GGCCCCGAAATGGAACCTCGAACAACACCTCTGGCATTGACTTCAAAACAGTTAACTTCC	733
Qy	743	TGAGGAAGCTTCAGAGAACTCACTCTGAGAGACTATGGAAGGGCCGCTGGCAGGGCAATG	802
Db	734	TGAGGAAGCTTCAGAGAACTCACTCTGAGAGACTATGGAAGGGCCGCTGGCAGGGCAATG	793
Qy	803	ACATTGTCGTAGAGGTGCTGAAGTTTGAGACTGAGACTACAGGAAGACAGGACCTTCA	862
Db	794	ACATTGTCGTAGAGGTGCTGAAGTTTGAGACTGAGACTACAGGAAGACAGGACCTTCA	853
Qy	863	ATGAAGAAGTCCCCCGGCTCAGAAATTTCTCGAATCCAAATGTGCTCCCACTGCTAGGTG	922
Db	854	ATGAAGAAGTCCCCCGGCTCAGAAATTTCTCGAATCCAAATGTGCTCCCACTGCTAGGTG	913
Qy	923	CCTGCGAGTCTCCACACTGCTCCTCATCTCATCTCACACACTGTGATGCGGTATGGAT	982
Db	914	CCTGCGAGTCTCCACACTGCTCCTCATCTCATCTCACACACTGTGATGCGGTATGGAT	973
Qy	983	CCCTCTACATGTACTACATGAGGACCAATTTGTCGTGAGACCAAGCCAGGCTGTGA	1042
Db	974	CCCTCTACATGTACTACATGAGGACCAATTTGTCGTGAGACCAAGCCAGGCTGTGA	1033
Qy	1043	AGTTTGCTTTGGAATGAGCAAGGGGCAATGGCTTCTCAACACACTGAGCCCTCAATCC	1102
Db	1034	AGTTTGCTTTGGAATGAGCAAGGGGCAATGGCTTCTCAACACACTGAGCCCTCAATCC	1093
Qy	1103	CACGACATGCACTCAATAGCCGTAGTGAATGATTTGATGAGACATGACTGCCGAATTA	1162
Db	1094	CACGACATGCACTCAATAGCCGTAGTGAATGATTTGATGAGACATGACTGCCGAATTA	1153
Qy	1163	GCAATGCTGATGTCAAGTCTCTTTCCAAATGCTCTGGTCTGCATGTATGCATCTGCTGGG	1222
Db	1154	GCAATGCTGATGTCAAGTCTCTTTCCAAATGCTCTGGTCTGCATGTATGCATCTGCTGGG	1213
Qy	1223	TAGCCCCCGAAGCTCTGCAAGAAAGCTGTAAGACACAAACAGCGCTCAGCAGACATGT	1282
Db	1214	TAGCCCCCGAAGCTCTGCAAGAAAGCTGTAAGACACAAACAGCGCTCAGCAGACATGT	1273
Qy	1283	GGAGTTTGGAGTGGCTTCTGTGGGAATGTGGTGAACAGGGAGGTACCCCTTTGCTGACCTCT	1342
Db	1274	GGAGTTTGGAGTGGCTTCTGTGGGAATGTGGTGAACAGGGAGGTACCCCTTTGCTGACCTCT	1333
Qy	1343	CCAAATATGAGATTGGAATGGAAGGTGCAATTGGAAGGCTTTGGCCTTACCATCCACACAG	1402
Db	1334	CCAAATATGAGATTGGAATGGAAGGTGCAATTGGAAGGCTTTGGCCTTACCATCCACACAG	1392
Qy	1403	GTAATTTCCCTCATGTGTGTAGCTCATGAAGATCTGCATGAATGAAGACCTTGCAAAAC	1462
Db	1393	GTAATTTCCCTCATGTGTGTAGCTCATGAAGATCTGCATGAATGAAGACCTTGCAAAAC	1452
Qy	1463	GACCCAAATTTGACATGATGTGTGCTATCTCTTGAAAGATGACAGAACAGTAGGAGACTGGA	1522
Db	1453	GACCCAAATTTGACATGATGTGTGCTATCTCTTGAAAGATGACAGAACAGTAGGAGACTGGA	1512
Qy	1523	AGGTCTTTCCTGCACTCAGAGGTGTGCGAGACATGGTTGGGGGAATGCATCTCCCAA	1582
Db	1513	AGGTCTTTCCTGCACTCAGAGGTGTGCGAGACATGGTTGGGGGAATGCATCTCCCAA	1572
Qy	1583	GCAGCAGGCTCTGTGGTGTGCTTCCCCCGCTTCACTATGTGTACTAACCCACAGCC-TGGGGT	1641
Db	1573	GCAGCAGGCTCTGTGGTGTGCTTCCCCCGCTTCACTATGTGTACTAACCCACAGCC-TGGGGT	1632

Db 841 CTACATGAGGACCAATTTGGTGTGACAGAGCAAGCTGTAAAGTTTGGCTTGGAC 900
Qy 1057 ATGGCAAGGGATGGCTTCTTACACACACTAGAGCCCTCATCCACGACATGCACTC 1116
Db 901 ATGGCAAGAGGATGGCTTCTTACACACACTAGAGCCCTCATACCTCGACATGCACTA 960
Qy 1117 AATAGCCCTAGTGTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1176
Db 961 AATAGCCCTAGTGTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
Qy 1177 AAGTTCTCTTCCCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1236
Db 1021 AAGTTCTCTTCCCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Qy 1237 CTGCAGAGAAGCTTGAAGACACAAAGAGCGCTCAGACAGATGTGGAGTTTTCAGTG 1296
Db 1081 CTGCAGAGAAGCTTGAAGACACAAAGAGCGCTCAGACAGATGTGGAGTTTTCAGTG 1140
Qy 1297 CTTCTGTGGGAAGCTTGAAGACACAAAGAGCGCTCAGACAGATGTGGAGTTTTCAGTG 1356
Db 1141 CTTCTGTGGGAAGCTTGAAGACACAAAGAGCGCTCAGACAGATGTGGAGTTTTCAGTG 1200
Qy 1357 GGAATGAAGGTGGCAATGGAAGGCTTCCGGCTTACCATCCACAGGTATTTCCCTCAT 1416
Db 1201 GGAATGAAGGTGGCAATGGAAGGCTTCCGGCTTACCATCCACAGGTATTTCCCTCAT 1260
Qy 1417 GTGTGTAAGCTTGAAGATCTGATGATGATGATGATGATGATGATGATGATGATGATG 1476
Db 1261 GTGTGTAAGCTTGAAGATCTGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Qy 1477 ATGATTGTGCTATCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATG 1515
Db 1321 ATGATTGTGCTATCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATG 1359

RESULT 8

ABL16569
ID ABL16569 standard; DNA; 1820 BP.
XX
AC ABL16569;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 1180.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 1180; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 1820 BP; 477 A; 417 C; 479 G; 447 T; 0 other;

Query Match 26.1%; Score 466.8; DB 23; Length 1820;
Best Local Similarity 60.2%; Pred. No. 9.3e-121;
Matches 812; Conservative 0; Mismatches 527; Indels 9; Gaps 2;
Qy 157 ATGACGACATTTTCACTCAGTCGCGGAGGCAACGAGTCGCGCTTGGCTGTGGCTG 216
Db 171 ATGAGGACATATCCACTGTGCGCGAGGCAACTCGATTCAAGTCGCGCTTGGTTG 230
Qy 217 GACAACCGGAGAACGACCTCAACAGGGGACGATCATGGCTTCTCCCTTGGACTGG 276
Db 231 GATGAACCGGAGCACGACAAATTTGGGAGACCACTGGCTTTCAGCCCTTGCATTGG 290
Qy 277 GCCTGCCGAGAGGCGCTCTGCTGTGTTGAGATGTTGATCATGCGGGGCGACGATC 336
Db 291 GTGGCTAAAGAGGCGCACGCCAAGCTTGTGGAGACTCTGTTGACGCGGTTCCGCTGTG 350
Qy 337 AATGTAATGAACCGTGGGGATGACACCCCTCGATCTGGCAGCGAGTCATGAGCACCGT 396
Db 351 AACGCCACCAATATGGCGGACGACATCCCACTCCATTTAGCGGAGCTCATGGCCACGC 410
Qy 397 GATATTGTACAGAAGCTATTGCAGTACAAGCGACACATCAATGCAAGTGAATGAACCGG 456
Db 411 GACGTGTCTCAGATGTTGATAAAAGAGCGGACGATGTGAATGCGGTAAACGAGCATGGA 470
Qy 457 AATGTCCTGTCACATGCTGCTGTTTGGGGCAAGATCAAGTGGCAGAGGACCTGGTG 516
Db 471 AACACCCCTGTCACCTAGCCTGTTTTTGGGGCTATGACATGATCTGGAGGATCTGCTT 530
Qy 517 GCAAATGGGCGCTTGTGACATCTGTAACAAGATATGGAGAGATCCCTTGTGGCAAAAGCC 576
Db 531 AATCGGAGGCCAGGTGGGAATCGCAAAACAGGACGGGCACACACCTCTTGAAGAGGCC 590
Qy 577 AAGGACCCCTGAGAGAGCTTCTCGAGAGCGGCGAGAGAGATGGCCAGCAATCTCAAC 636
Db 591 AAACCCAGTCTGGCCAAAGAGGCTTTCAGGATCTTGTAGAAAAGAGCGGACAGAGGTTAAG 650
Qy 637 CGTATTCCATACAAGGACACATCTGGAAGGGGACCCCGCCTCGSCCCGGAATGGA 696
Db 651 GTTATCAGCTTCAAGGAACAAGCTGGCAGGATTTGAAG---ACGAGATCCCGGATGCT 707
Qy 697 ACCCTGAACAAACACTCTGGCAITGACTTCAACAGCTTAACTTCTTGACGAAGCTCAAC 756
Db 708 ACTTTGTCCCGTTTCAAGGGAATCAGTATGGAGACCTTAGACCTGCATACCAAGTGTG 767
Qy 757 GAGAACTACTCTGAGAGCTTATGGAAGCGCGCTGGCAGGGCAATGACATTTGCTGTAAG 816
Db 768 GTGACGCCATCAGGAGAACTTGGCGCGGACGCTGGCAAAAAGAACGATGTGTAGCTAAG 827
Qy 817 GTGCTGAAGGTTTCGAGACTGGAGTACAAGGAAGACGAGGACTTCAATGAAGAGTGTCCC 876
Db 828 ATCTGGCCGTGCTCAGTGCACGCTCGTATATCGCGAGATTTTAAAGAGAGTTTCCC 887
Qy 877 CGGCTCAGGATTTTCTCGCATCCAAATGTGCTCCAGTGTAGTGGCTGCGAGTCTCCA 936
Db 888 AAGCTCGCATCTTTTTCGACCCCTAAACATTTTGGCTATTATTGGAGCATGCAATTCGCA 947
Qy 937 CCTGCTCTCATCTACTCTCATCACACACTGGATGCGGTATGGATCCCTACATATGA 996
Db 948 CCCAATCTGGTGACAATT-----AGTCAGTTTATGCCACGTTCTTCGCTGTGTTAGCGCTG 1001


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RESULT 10
AAA78148/c
ID AAA78148 standard; cDNA; 330 BP.
XX
AC AAA78148;
XX
XX 14-NOV-2000 (first entry)
DT
DE cDNA encoding human colon tumour polypeptide, SEQ ID NO:435.
XX
XX Human colon tumour polypeptide; tumour antigen; cancer; vaccine;
KW immunotherapy; diagnosis; progression; ss.
XX
XX Homo sapiens.
OS
XX WO200037643-A2.
XX
XX 29-JUN-2000.
XX
XX 23-DEC-1999; 99WO-US30909.
XX
XX 23-DEC-1998; 98US-0221298.
XX
XX 02-JUL-1999; 99US-0347496.
XX
XX 22-SEP-1999; 99US-0401064.
XX
XX 19-NOV-1999; 99US-0444242.
XX
XX 02-DEC-1999; 99US-0454150.
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk J;
PI Wang T, Yuqiu J;
XX
XX WPI; 2000-442671/38.
XX
XX New colon tumor polypeptides used to inhibit the development of cancer,
PT especially colon cancer, and for diagnosing and monitoring the
PT progression of the cancer -
XX
XX Claim 1; Page 216; 229pp; English.
XX
XX Sequences AAA7722-A78199 represent 478 cDNAs encoding proteins or
XX portions of proteins which are associated with human colon tumours.
XX The invention also specifically discloses 8 human colon tumour proteins
XX (AAB1197-B11904). The nucleic acids, the polypeptides they encode, and
XX such polypeptides may be used in vaccines that target tumour cells,
XX especially colon tumour cells, thereby inhibiting the development of
XX cancer. T-cells specific for the polypeptide expressed by the APC are
XX used to remove tumour cells from biological samples, especially blood or
XX fractions thereof. The sample or the isolated T-cells specific for the
XX polypeptide can then be used to inhibit cancer development. CD4+ and/or
XX CD8+ T-cells from a patient may be incubated with a polypeptide or
XX nucleic acid of the invention, or an APC expressing such a polypeptide,
XX to cause the proliferation of specific T-cells. The T-cells can be
XX cloned and then administered back to the patient to inhibit cancer
XX development. Nucleic acids encoding the polypeptides and antibodies
XX against the polypeptides may be used to determine the expression level
XX of a tumour protein of the invention, and therefore to determine whether
XX cancer cells are present. Such diagnostic methods may also be used to
XX monitor the progression of a cancer by repeating the processes at time
XX intervals, and comparing the current result to previous results. The
XX present sequence represents a cDNA encoding a human colon tumour
XX polypeptide.
XX
XX Sequence 330 BP; 76 A; 89 C; 83 G; 82 T; 0 other;
SQ
Query Match 18.4%; Score 328.4; DB 21; Length 330;
Best Local Similarity 99.7%; Pred No. 3.9e-82;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 996 ACTACATGAAGGCACCAATTTGCTGGACGAGCCAGCTGTGAAGTTTGCTTTGGA 1055
|||||
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CC patients own production of them. Additionally, (II) may be used to
CC produce the TCAP proteins, by inserting the nucleic acids into a host
CC cell culturing the cell to express the protein. (II) and (I) in diagnostic
CC complementary sequences may also be used as DNA probes in diagnostic
CC polymerase chain reaction (PCR) and hybridization assays to detect and
CC quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. (I) may
CC also be used as antigens in the production of antibodies against TCAPs
CC and in assays to identify modulators of TCAP expression and activity.
CC Anti-(I) antibodies and antagonists may also be used to down regulate
CC TCAP expression and activity. The anti-(I) antibodies may also be used
CC as diagnostic agents for detecting the presence of TCAPs in samples
CC (e.g. by enzyme linked immunosorbent assay (ELISA)). AA128460 to AA129512
CC and AA24494 to AA24523 represent nucleotide and amino acid sequences
CC given in the exemplification of the present invention.

XX Sequence 330 BP; 76 A; 89 C; 83 G; 82 T; 0 other;

Query Match 18.4%; Score 328.4; DB 22; Length 330;

Best Local Similarity 99.7%; Pred. No. 3.9e-82; Mismatches 1; Indels 0; Gaps 0;

Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 996 ACTACATGAAGGACCAATTGCTGTGAGCAGAGCCAGGCTGTGAAGTTGCTTTGA 1055
Db 330 ACTACATGAAGGACCAATTGCTGTGAGCAGAGCCAGGCTGTGAAGTTGCTTTGA 271
Qy 1056 CATGCAAGGGGCGATGCGCTTCTACACACTAAGCCCTCATCCACGACATGCACT 1115
Db 270 CATGCAAGGGGCGATGCGCTTCTACACACTAAGCCCTCATCCACGACATGCACT 211
Qy 1116 CAATGCGGTAGTGAATGATGATGAGACATGACTGCGCAATTAGCATGGCTGATGT 1175
Db 210 CAATGCGGTAGTGAATGATGATGAGACATGACTGCGCAATTAGCATGGCTGATGT 151
Qy 1176 CAAGTTCTCTTCCATGTCCTGTCGATGTATGCACTGCTGGGTAGCCCGGAAGC 1235
Db 150 CAAGTTCTCTTCCATGTCCTGTCGATGTATGCACTGCTGGGTAGCCCGGAAGC 91
Qy 1236 TCTGCAAGAAAGCCTGAAGACAAACAGAGCCTCAGACAGCATGTGTGAGTTTGCAGT 1295
Db 90 TCTGCAAGAAAGCCTGAAGACAAACAGAGCCTCAGACAGCATGTGTGAGTTTGCAGT 31
Qy 1296 GCTTCTGTGGAACTGTGACACGGGAGGT 1325
Db 30 GCTTCTGTGGAACTGTGACACGGGAGGT 1

RESULT 12
ABZ33072/C
ID ABZ33072 standard; cDNA; 330 BP.

XX ABZ33072;

DT 30-JAN-2003 (first entry)

XX Human colon tumour cDNA clone 32010 SEQ ID NO:435.

KW Human; colon cancer; colon tumour; immunotherapy; diagnosis; cancer;
KW tumour; immune response; immunostimulant; cytostatic; vaccine;
KW gene; ss.

XX Homo sapiens.

XX WO200283070-A2.

XX 24-OCT-2002.

XX 09-APR-2002; 2002MO-US11475.

XX 10-APR-2001; 2001US-0833263.

XX 03-AUG-2001; 2001US-0922217.

XX 19-DEC-2001; 2001US-0025380.

PA (CORI-) CORIXA CORP.

XX Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk JA;

PI Wang T, Jiang Y, Smith CU, King GE, Wang A, Clapper JD;

PI Skelky YAW, Fanger GR, Vedvick TS, Carter D;

XX WPI; 2003-067548/06.

PS Example 1; Page 255-256; 537pp; English.

CC The present invention describes compounds (I) for the immunotherapy and
CC diagnosis of colon cancer. Also described: (1) a method for detecting and/or
CC the presence of cancer in a patient; (2) a method for stimulating and/or
CC expanding T cells specific for a tumour protein; (3) an isolated T cell
CC population comprising T cells prepared by the method of (2); (4) a method
CC for stimulating an immune response in a patient; (5) a method for
CC treating cancer in a patient; and (6) a method for inhibiting the
CC development of cancer in a patient. (I) have immunostimulant and
CC cytostatic activities and can be used in vaccines. ABZ32646 to ABZ33725
CC and ABP55343 to ABP55391 represent human colon cancer/tumour related
CC sequences used in the exemplification of the present invention.

XX Sequence 330 BP; 76 A; 89 C; 83 G; 82 T; 0 other;

Query Match 18.4%; Score 328.4; DB 25; Length 330;

Best Local Similarity 99.7%; Pred. No. 3.9e-82; Mismatches 1; Indels 0; Gaps 0;

Qy 996 ACTACATGAAGGACCAATTGCTGTGAGCAGAGCCAGGCTGTGAAGTTGCTTTGA 1055
Db 330 ACTACATGAAGGACCAATTGCTGTGAGCAGAGCCAGGCTGTGAAGTTGCTTTGA 271
Qy 1056 CATGCAAGGGGCGATGCGCTTCTACACACTAAGCCCTCATCCACGACATGCACT 1115
Db 270 CATGCAAGGGGCGATGCGCTTCTACACACTAAGCCCTCATCCACGACATGCACT 211
Qy 1116 CAATGCGGTAGTGAATGATGATGAGACATGACTGCGCAATTAGCATGGCTGATGT 1175
Db 210 CAATGCGGTAGTGAATGATGATGAGACATGACTGCGCAATTAGCATGGCTGATGT 151
Qy 1176 CAAGTTCTCTTCCATGTCCTGTCGATGTATGCACTGCTGGGTAGCCCGGAAGC 1235
Db 150 CAAGTTCTCTTCCATGTCCTGTCGATGTATGCACTGCTGGGTAGCCCGGAAGC 91
Qy 1236 TCTGCAAGAAAGCCTGAAGACAAACAGAGCCTCAGACAGCATGTGTGAGTTTGCAGT 1295
Db 90 TCTGCAAGAAAGCCTGAAGACAAACAGAGCCTCAGACAGCATGTGTGAGTTTGCAGT 31
Qy 1296 GCTTCTGTGGAACTGTGACACGGGAGGT 1325
Db 30 GCTTCTGTGGAACTGTGACACGGGAGGT 1

RESULT 13
ABL16568

ID ABL16568 standard; DNA; 4354 BP.

XX ABL16568;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 1177.

KW Drosophila; developmental biology; cell signalling; insecticide;

KW pharmaceutical; gene; ds.

XX Drosophila melanogaster.

XX WO200171042-A2.

PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX
PS Claim 1; SEQ ID NO 1177; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 4354 BP; 1223 A; 902 C; 945 G; 1284 T; 0 other;

Query Match 17.0%; Score 305; DB 23; Length 4354;
Best Local Similarity 56.8%; Pred. No. 5.4e-75;
Matches 642; Conservative 0; Mismatches 430; Indels 59; Gaps 2;

QY 430 GACATCAATGAGTGAACACGGGAATGTGCCCTGCACTATGCTGTTTGGGCG 489
DB 1916 GATGTGAATGCGGTNAACAGCATGGAACACCCCTGCACTACGCTGTTTGGGCG 1975

QY 490 CAAGATCAAGTGGCAGAGACCTGTGTGCAAAATGGGCGCCCTTGTGAGCATCTGTAACAAG 549
DB 1976 TATGACATGATCTGCGAGGATCTGCTTAATGCGGGAGCCAGGTGGGAATCGCAACAAG 2035

QY 550 TATGAGAGATGCTGTGTGCAAAAGCCCAAGGACCCCTGAGAGAGCTTCTCGAGAGCGG 609
DB 2036 GACGGGCACACACCTCTTTGAAAGGCCCAACCCAGTCTGGCCAAAGAGGCTTCAGGATCTT 2095

QY 610 GCAGAGAAGATGGGCCAGAACTCTCAACCGTATTCCATACAAGGACACATTTCTGGAAGGGG 669
DB 2096 GTAGAAAAGAGCGGCAGAGAGGTTAAGGTTATCAGCTTCAAGGAACAAGTGGCAGGGA 2155

QY 670 ACCACCCGCACTCGGCCCCCGAAATGGAAACCTGTGAACAAACACTCTGGCAATTGACTTCAAA 729
DB 2156 TTGA---AGACGAGATCCCGGATGCTACTTTGTCCCGTTTCAAGGGAATCAGTATGGA 2212

QY 730 CAGCTTAATCTCTGACGAAGCTCAACGAGAAATCACTCTGGAGAGCTATGGAAGGCCGCG 789
DB 2213 GACCTAGACCTGCATACCAGCTGTGCGGTGACGCCATCAGGAGAACTTGGCGCGGACGC 2272

QY 790 TGGCAGGGCAATGACATTTGCTGTAAGGTGCTGAAGGTTTCGAGACTGGAGTACAAGGAAG 849
DB 2273 TGGGCAAAAGACGATGTGGTGTAGTGAATCTTGGCCGTGCGTCACTGACGCCCTCGTATA 2332

QY 850 AGCAGGGACTTCAATGAAGAGTGTCCCGGCTCAGGATTTTCTCGCATCCAAATGTGCTC 909
DB 2333 TCGCGAGATTTTAACGAGGAGTTTCCCAAGCTTCGCACTCTTTTCGCAACCTTAACATTTG 2392

QY 910 CCAGTGTAGTGTGCTGCGAGTCTCCACCTGCTC----- 943
DB 2393 CCTATTATTGGAGCATGCAATTCGCCCAACCACTCTGGTGACAATTTAGTCAGGTGCGTTGA 2452

QY 944 -----CTCATCTACTCTCATCACACATGGATGC 973
DB 2453 ATTTAAATACTTCAGAAATGACCGTATAAGGTAAACCATCTATTCTTTTAGTTATGC 2512

QY 974 CGTATGGATCCCTCTCAATGTACTACATGAAGCACAATTTCTGTCGTGACAGAGCC 1033
DB 2513 CACGTTCTTCTGCTGTTAGCCTGTCATGAGCAACTGGCGTCTGTTGTCGACACAGCC 2572

QY 1034 AGGCTGTCAAGTCTTGGCATGCAAGGGCATGGCTTCTCTACACACATAGAGC 1093
DB 2573 AGCGGTAAAGCTTTGCTTGGATGTTGCGAGAGAAATGGCTTCTCTGACCTCGTGGAGC 2632

QY 1094 CCCTCATCCACAGCATGCACTCAATAGCCGTAGTAAATGATTGATGAGGACATGACTG 1153
DB 2633 GCATTATTCCAAATATACCTGAAACAGTCACTACGCTGATGATCGACGATCTGACGG 2692

QY 1154 CCCGAATTAGCATGGCTGATGTCAGTCTCTTCCAAATGCTCTGGTCGCAATGTATGCAC 1213
DB 2693 CGAGAATCAACATGGCGGATGCCAAATTTCTTTTCCAAGAGAGGAGCGCATCTATCAAC 2752

QY 1214 CTGCTGGGTAGCCCCCGAAGCTCTGCAGAGAGCCCTGAAGACACAACAGACGCTCAG 1273
DB 2753 CGGCTTGGATGTCGCCCGAAACATTTGACGCGCAAGCAGGCGGATCGAAACTGGAGGCT 2812

QY 1274 CAGACATGTGGAGTCTTGTGCAAGTCTCTGTGGGAACCTGGTGACACGGGAGGTACCTTTG 1333
DB 2813 GTGACATGTGGAGCTTTGCTATTCTTTTGGGAGCTGACTACGCGGAGGTACCTTCG 2872

QY 1334 CTGACCTCTCAATATGAGAGATTTGGAATGAAGTGGCATTTGGAAGGCTTTCGGCTTACCA 1393
DB 2873 CCGAGTGTGTCGCCCATGGAGTGGCGCATGAAAATTTGGTTTGGAAAGGTCTGGGGTCAAGA 2932

QY 1394 TCCACACAGGATTTTCCCTCATGCTGTGAAGCTCATGAGATCTGCAATGATGAAGACC 1453
DB 2933 TTCCGCCAGGACATCGACGCAATGGCCAAAGCTGATTTCAATCTGATGAACGAGGATC 2992

QY 1454 CTGCAAAAGCGACCCAAATTTGACATGATTTGTCCTATCTCTTGGAAAGATGC 1504
DB 2993 CCGGCAAGGCGCCCAAGTTCGACATGTTGGTTTCCCATTTCTGGAGAAGATGC 3043

RESULT 14
AAH35546
ID AAH35546 standard; cDNA; 568 BP.
XX
AC AAH35546;
XX
DT 03-SEP-2001 (first entry)
XX
Human colon cancer antigen encoding cDNA SEQ ID NO:2628.
XX
DE Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; chromosome 11; ss.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
XX WPI; 2001-235357/24.
DR P-PSDB; AAG76141.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,

PT useful for preventing, diagnosing and/or treating colorectal cancers -
 XX
 PS Claim 1: Page 4235-4236; 9803pp; English.

CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate P
 CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing
 CC inactive proteins or to supplement the patient's own production of P.
 CC Additionally, N may be used to produce the colon cancer-associated P,
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 CC and AAG77789 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.

SO Sequence 568 BP; 148 A; 136 C; 143 G; 129 T; 12 other;

Query Match 13.5%; Score 240.8; DB 22; Length 568;
 Best Local Similarity 97.2%; Pred. No. 2.4e-57;
 Matches 245; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 451 CACGGGAATGTCCTCCATCATGCTGTTTGGGGCAAGATCAAGTGGCAGAGGC 510
 Db 2 CACGGGAATGTCCTCCATCATGCTGTTTGGGGCAAGATCAAGTGGCAGAGGC 61
 OY 511 CTGTGGCAATGGGGCCCTTGTGCAATCTGTAAACAAGTATGAGAGTGGCTGTGAC 570
 Db 62 CTGTGGCAATGGGGCCCTTGTGCAATCTGTAAACAAGTATGAGAGTGGCTGTGAC 121
 OY 571 AAAGCCAGGCAAGCCCTTGTGAGAGCTTCTCCAGAGCGGGCAGAGAAGTGGGCCAGAA 630
 Db 122 AAAGCCAGGCAAGCCCTTGTGAGAGCTTCTCCAGAGCGGGCAGAGAAGTGGGCCAGAA 181
 OY 631 CTCACCGTATTCATACAGAGACATTCCTGGAAGGGGACACCCGCACTGGCCCGCA 690
 Db 182 CTCACCGTATTCATACAGAGACATTCCTGGAAGGGGACACCCGCACTGGCCCGCT 241
 OY 691 AATGGAACTCTG 702
 Db 242 GAGTCACCACTG 253

RESULT 15
 ABX74732/C
 ID ABX74732 standard; cDNA; 285 BP.

XX AC ABX74732;

XX DT 21-MAR-2003 (first entry)

DE Human cDNA sequence #55 differentially expressed in CC-RCC types.

XX Human; microarray; solid surface; immobilised probe; CC-RCC;
 KW differential expression profile; aggressive CC-RCC tumour type;
 KW non-aggressive CC-RCC tumour type; clear cell renal carcinoma;
 KW gene expression profiling; tumour tissue; gene; ss.

OS Homo sapiens.

XX PN WO200279411-A2.

XX PD 10-OCT-2002.

XX PF 29-MAR-2002; 2002MO-US09576.

XX 29-MAR-2001; 2001US-279411P.
 PR
 XX (VAND-) VAN ANDEL INST.
 PA
 XX Haab B, Rhodes D, Teh BT, Takashi M;
 PI
 XX WPI; 2003-040679/03.

DR
 XX
 PT New microarray, comprising a matrix of cDNA probe from a set of probes
 PT immobilised to a solid surface in predetermined order, useful in the
 PT prognosis of patients with clear cell renal carcinoma -
 PS Claim 1: SEQ ID No 386; 179pp; English.

XX The present invention relates to a microarray comprising a matrix of
 CC at least one cDNA probe from a set of probes immobilised to a solid
 CC surface in a predetermined order, where a row of pixels corresponds
 CC to replicates of one distinct probe from the set. The probes are
 CC complementary to nucleic acid sequences that are expressed
 CC differentially in aggressive as compared to non-aggressive types of
 CC clear cell renal carcinoma (CC-RCC) and that hybridise to the probes
 CC under high stringency conditions. The microarray is useful for the
 CC prognosis of patients with CC-RCC, wherein aggressive and
 CC non-aggressive CC-RCC tumour types are characterised by differential
 CC expression profiles of genes that hybridise with one or more probes
 CC immobilised on the microarray. The arrays are useful for gene
 CC expression profiling of tumour and normal tissues. The present
 CC sequence represents a human cDNA sequence differentially expressed
 CC in aggressive vs. non-aggressive type CC-RCC phenotypes.

SO Sequence 285 BP; 57 A; 72 C; 86 G; 66 T; 4 other;

Query Match 12.8%; Score 228.8; DB 25; Length 285;
 Best Local Similarity 97.4%; Pred. No. 4.1e-54;
 Matches 263; Conservative 0; Mismatches 4; Indels 3; Gaps 3;

OY 1513 TAGACCTGGAAGGTCCTTTCCTGAATCCAGAGGTGCGGACATGTTGGGGAAATGC 1571
 Db 270 TAGACCTGGAAGGTCCTTTCCTGAATCCAGAGGTGCGGACATGTTGGGGAAATGC 211
 OY 1572 ACCTCCCAAGAGCAGAGGCTTGTGCTCTCCGCCCTTCACTGATGTAATACCC 1631
 Db 210 ACCTCCCAAGAGCAGAGGCTTGTGCTCTCCGCCCTTCACTGATGTAATACCC 151
 OY 1632 AGCC-TGGGGTCCATCCCTTCCCATCCCTTACCACTGT-GCGCAAGAGGGCGGCTC 1689
 Db 150 AGCCATGGGGTCCATCCCTTCCCATCCCTTACCACTGTGCGCAAGAGGGCGGCTC 91
 OY 1690 AGAGCTTTGACTCTGCAATGATGTTCTCCCAATATGGAGGATCAAGCCCGCTGTC 1749
 Db 90 AGAGCTTTGACTCTGCAATGATGTTCTCCCAATATGGAGGATCAAGCCCGCTGTC 31
 OY 1750 ACAATTAAGTTTATTAATAAAAAA 1779
 Db 30 ACAATTAAGTTTATTAATAAAAAA 1

Search completed: September 22, 2003, 17:14:38
 Job time : 374 secs

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Query Match	100.0%	Score 1789	DB 3	Length 1789
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1789	Conservative 0	Mismatches 0	Indels 0	Gaps 0

1 GAAATTCATCTGTCGACTGCTTACACGGGAGTTCCCGGAGAGGATCCTGAGCCCGAGT 60
Db
1 GAAATTCATCTGTCGACTGCTTACACGGGAGTTCCCGGAGAGGATCCTGAGCCCGAGT 60
Qy
61 CCCGAGGATAAAGCTTTGGGGTTATCTCTCTTCCCTGGATCACTCCACAGTCTCAGGCT 120
Db
61 CCCGAGGATAAAGCTTTGGGGTTATCTCTCTTCCCTGGATCACTCCACAGTCTCAGGCT 120
Qy
121 TCCCAATCCAGGGGACTCGGGCCGGGACGCTGCTATGGACGACATTTTCACTCAGTGC 180
Db
121 TCCCAATCCAGGGGACTCGGGCCGGGACGCTGCTATGGACGACATTTTCACTCAGTGC 180
Qy
181 CGGAGGGCAACGAGTCCGCTTTCGCTTGGCTGGACAACACGAGAAACGACTCAAC 240
Db
181 CGGAGGGCAACGAGTCCGCTTTCGCTTGGCTGGACAACACGAGAAACGACTCAAC 240
Qy
241 CAGGGGACGATCATGCTTTCCTCCCTTTCGCTTGGCTGGACAACGAGGGCCGCTTGCCT 300
Db
241 CAGGGGACGATCATGCTTTCCTCCCTTTCGCTTGGCTGGACAACGAGGGCCGCTTGCCT 300
Qy
301 GTGTTGAGATGTTGATCATCGGGGGGACGAGTCAATGTAATGAACCGTGGGATGAC 360
Db
301 GTGTTGAGATGTTGATCATCGGGGGGACGAGTCAATGTAATGAACCGTGGGATGAC 360
Qy
361 ACCCCCTGCTATCGGACGAGTCAATGTAATGAACCGTGGGATGAC 420
Db
361 ACCCCCTGCTATCGGACGAGTCAATGTAATGAACCGTGGGATGAC 420
Qy
421 TACAAGGAGACATCAATGAGTGAATGAACACGAGGATGTCCTTGCATATGCTTGT 480
Db
421 TACAAGGAGACATCAATGAGTGAATGAACACGAGGATGTCCTTGCATATGCTTGT 480
Qy
481 TTTTGGGGCCAGATCAAGTGGCAGAGACCTGTCGCAATGGGCGCTTGTGAGATC 540
Db
481 TTTTGGGGCCAGATCAAGTGGCAGAGACCTGTCGCAATGGGCGCTTGTGAGATC 540
Qy
541 TGTAACAGTATGGAGAGATGCTTGGACAAGCCAGGACCCCTCGAGAGAGCTTCTC 600
Db
541 TGTAACAGTATGGAGAGATGCTTGGACAAGCCAGGACCCCTCGAGAGAGCTTCTC 600
Qy
601 CGAGAGCGGAGAGAGATGGCCAGAAATCTCAACCGTATTCATCAAGAGACACATTC 660
Db
601 CGAGAGCGGAGAGAGATGGCCAGAAATCTCAACCGTATTCATCAAGAGACACATTC 660
Qy
661 TGGAGGGGACCCCGCAGTCCGCGGAGTGAACCGTGAACACATCTTGGCAT 720
Db
661 TGGAGGGGACCCCGCAGTCCGCGGAGTGAACCGTGAACACATCTTGGCAT 720
Qy
721 GACTTCAACAGCTTAACTTCTGACGAGCTCAACGAGATCACTCTGGAGAGCTATGG 780
Db
721 GACTTCAACAGCTTAACTTCTGACGAGCTCAACGAGATCACTCTGGAGAGCTATGG 780
Qy
781 AAGGCCCTGCGAGGGCAATGACATTTCTGTAAGTGTCTGAAGTTTCGAGACTGGAGT 840
Db
781 AAGGCCCTGCGAGGGCAATGACATTTCTGTAAGTGTCTGAAGTTTCGAGACTGGAGT 840
Qy
841 ACAAGGAGACGAGGACTTCAATGAAGTGTCTCCCGCTCAGATTTTCTCGCATCCA 900
Db
841 ACAAGGAGACGAGGACTTCAATGAAGTGTCTCCCGCTCAGATTTTCTCGCATCCA 900
Qy
901 AATGTCTCCAGAGTCTAGGTGCTTCCAGTCTCCACCTGCTCTCTCTCTCTCTCTCT 960
Db
901 AATGTCTCCAGAGTCTAGGTGCTTCCAGTCTCCACCTGCTCTCTCTCTCTCTCTCT 960
Qy
961 ACACACTGGATGCGGTATGATTCCTCTCAATGTAATGTAAGGACCAATTTTCTCT 1020
Db
961 ACACACTGGATGCGGTATGATTCCTCTCAATGTAATGTAAGGACCAATTTTCTCT 1020
Qy
1021 GTGACACGAGCCGAGCTGAGTTTCTTGGACATGGCAAGGGGATGCTTCTCTCT 1080
Db
1021 GTGACACGAGCCGAGCTGAGTTTCTTGGACATGGCAAGGGGATGCTTCTCTCTCT 1080
Qy
1081 CACACACTAGAGCCCTCTATCCACGACATGCACTCAATAGCCGCTAGTGTATGATGAT 1140

1081 CACACACTAGAGCCCTCTATCCACGACATGCACTCAATAGCCGCTAGTGTATGATGAT 1140
Qy
1141 GAGGACATGATGCTCCCGAATTTAGCATGGCTGATGTCAGTTCTCTTTCCAAATGCTCGT 1200
Db
1141 GAGGACATGATGCTCCCGAATTTAGCATGGCTGATGTCAGTTCTCTTTCCAAATGCTCGT 1200
Qy
1201 CGCATGTATGACACCTGCTGGTAGCCCGGAGCTCTGAGAGAAAGCCCTGGAAGACACA 1260
Db
1201 CGCATGTATGACACCTGCTGGTAGCCCGGAGCTCTGAGAGAAAGCCCTGGAAGACACA 1260
Qy
1261 AACAGACGCTCAGCAGACATGTTGAGTGTTCAGTGTCTTGTGGGAACCTGGTGACACGG 1320
Db
1261 AACAGACGCTCAGCAGACATGTTGAGTGTTCAGTGTCTTGTGGGAACCTGGTGACACGG 1320
Qy
1321 GAGTACCTTTGCTGACCTCTCAATATGAGATTTGGAATGAAGTGGCATTTGGAAGGC 1380
Db
1321 GAGTACCTTTGCTGACCTCTCAATATGAGATTTGGAATGAAGTGGCATTTGGAAGGC 1380
Qy
1381 CTTCCGGCTACCATCCACAGAGTATTTCCCTCATGTGTGTAAGCTCATGAAGATCTGC 1440
Db
1381 CTTCCGGCTACCATCCACAGAGTATTTCCCTCATGTGTGTAAGCTCATGAAGATCTGC 1440
Qy
1441 ATGAATGAAGACCTTGCACACGACCCAAATTTGACATGATTTGCTCTATCTTTGAGAAG 1500
Db
1441 ATGAATGAAGACCTTGCACACGACCCAAATTTGACATGATTTGCTCTATCTTTGAGAAG 1500
Qy
1501 ATGAGAGCAAGTAGGACTGGAAGTCTTGCCTGAACTCCAGAGGTGTCGGGACATGGT 1560
Db
1501 ATGAGAGCAAGTAGGACTGGAAGTCTTGCCTGAACTCCAGAGGTGTCGGGACATGGT 1560
Qy
1561 TGGGGGAATGACCTTCCCAAGCAGAGGCTCTGTTGCTCTCCCGCTTCCAGTCTAT 1620
Db
1561 TGGGGGAATGACCTTCCCAAGCAGAGGCTCTGTTGCTCTCCCGCTTCCAGTCTAT 1620
Qy
1621 GGTACTACCCAGCTGGGTCTCATCCCTTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 1680
Db
1621 GGTACTACCCAGCTGGGTCTCATCCCTTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 1680
Qy
1681 GCGGGCTCAGAGCTTTGTACCTTCCACATGTTCTCCCAATGTTGCGCAAGAGG 1740
Db
1681 GCGGGCTCAGAGCTTTGTACCTTCCACATGTTCTCCCAATGTTGCGCAAGAGG 1740
Qy
1741 CCGCTGTCAATAAAGTTTATTAAGAAAAAAGAAAAAAGAAAAA 1789
Db
1741 CCGCTGTCAATAAAGTTTATTAAGAAAAAAGAAAAAAGAAAAA 1789

RESULT 2

US-08-955-841-1
; Sequence 1, Application US/08955841
; Patent No. 6013782

; GENERAL INFORMATION:

; APPLICANT: Dedhar, Shoukat
; APPLICANT: Hannigan, Greg
; TITLE OF INVENTION: Integrin-Linked Kinase and
; TITLE OF INVENTION: its Uses
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic and Reed, LLP
; STREET: 285 Hamilton Avenue, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,841
; FILING DATE:

CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: KIN-2C1P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650-327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1789 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-955-841-1

Query Match 100.0%; Score 1789; DB 3; Length 1789;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1789; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 GAATTCATCTGTCGACTGCTACCAAGGAGTCCCGGAGAGATCCTGACGCCGAGT 60
DB 1 GAATTCATCTGTCGACTGCTACCAAGGAGTCCCGGAGAGATCCTGACGCCGAGT 60
QY 61 CCCGAGGATTAAGCTTGGGGTTCATCTCTCTCCCTGATCACTCACAGTCTGAGGT 120
DB 61 CCCGAGGATTAAGCTTGGGGTTCATCTCTCTCCCTGATCACTCACAGTCTGAGGT 120
QY 121 TCCCAATTCAGAGGGACTGCGGCGCCGGGAGCGTGTATGAGACGACATTTTCACTGATGC 180
DB 121 TCCCAATTCAGAGGGACTGCGGCGCCGGGAGCGTGTATGAGACGACATTTTCACTGATGC 180
QY 181 CCGGAGGCGCAACGCACTGCGCCCTTGGCTGTGTGACACACGAGAGAACCACTCAAC 240
DB 181 CCGGAGGCGCAACGCACTGCGCCCTTGGCTGTGTGACACACGAGAGAACCACTCAAC 240
QY 241 CAGGGGAGCATCATGAGCTTCTCCCTTGCACCTGGGAGCTGCGAGAGGGCGCTCTGCT 300
DB 241 CAGGGGAGCATCATGAGCTTCTCCCTTGCACCTGGGAGCTGCGAGAGGGCGCTCTGCT 300
QY 301 GTGATTGAGATGTTGATCATGCGGGGGGCGAGATCAATGTATGAACCGTGGGATGAC 360
DB 301 GTGATTGAGATGTTGATCATGCGGGGGGCGAGATCAATGTATGAACCGTGGGATGAC 360
QY 361 ACCCCCTGCTATCTGCGACGCGCATGTAGACACCGTATATTGTACAGAGCTATTGCG 420
DB 361 ACCCCCTGCTATCTGCGACGCGCATGTAGACACCGTATATTGTACAGAGCTATTGCG 420
QY 421 TACAGGCGAGCATCAATGCAATGCAATGAACACGGAATGCCCCCTGACTATGCGTGT 480
DB 421 TACAGGCGAGCATCAATGCAATGCAATGAACACGGAATGCCCCCTGACTATGCGTGT 480
QY 481 TTTTGGGGCCAAAGATCAAGTGGCAAGAGACCTGTGGCAAAATGGGGCCCTTTGTACAGATC 540
DB 481 TTTTGGGGCCAAAGATCAAGTGGCAAGAGACCTGTGGCAAAATGGGGCCCTTTGTACAGATC 540
QY 541 TGTAACTAATATGAGAGATGCTGTGCAAAAGCCAAAGCCACCCCTGAGAGAGCTTCTC 600
DB 541 TGTAACTAATATGAGAGATGCTGTGCAAAAGCCAAAGCCACCCCTGAGAGAGCTTCTC 600
QY 601 CGAGAGCGGGGAGAGAGATGGGGCCGAAATCTCAACCGTATTCATACAGAGACATTC 660
DB 601 CGAGAGCGGGGAGAGAGATGGGGCCGAAATCTCAACCGTATTCATACAGAGACATTC 660
QY 661 TGGAAAGGGGACACCGGCACTGGGCGCCGAAATGGAACCTGTAACCACTCTGGCATT 720
DB 661 TGGAAAGGGGACACCGGCACTGGGCGCCGAAATGGAACCTGTAACCACTCTGGCATT 720
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QY 721 GACTTCAACAGACTTAATCTCTGACGAGGCTCAACGAAATCACTGAGAGCTATGG 780
DB 721 GACTTCAACAGACTTAATCTCTGACGAGGCTCAACGAAATCACTGAGAGCTATGG 780
QY 781 AAGGGCCGCTGGCAGGGCAATGACATTTGCGTGAAGTGTCTGAAGTTTGGAGCTTGAGT 840
DB 781 AAGGGCCGCTGGCAGGGCAATGACATTTGCGTGAAGTGTCTGAAGTTTGGAGCTTGAGT 840
QY 841 ACAAGGAAGAGCAGGAGCTTCAATGAGAGTGTCCCGGCTCAGAGATTTTCTGGATCCA 900
DB 841 ACAAGGAAGAGCAGGAGCTTCAATGAGAGTGTCCCGGCTCAGAGATTTTCTGGATCCA 900
QY 901 AATGCTCCCAAGTGTGATGAGTCCCTCTCAATATGACTATGAGAGGACCAATTTGCT 960
DB 901 AATGCTCCCAAGTGTGATGAGTCCCTCTCAATATGACTATGAGAGGACCAATTTGCT 960
QY 961 ACACACTGATGCTCCGATGATATCCCTCTCAATATGACTATGAGAGGACCAATTTGCT 1020
DB 961 ACACACTGATGCTCCGATGATATCCCTCTCAATATGACTATGAGAGGACCAATTTGCT 1020
QY 1021 GTGACACGAGCAGGCTGTGAAGTTTGTGACATGCGCAAGGGGCGATGGCTTCTCTA 1080
DB 1021 GTGACACGAGCAGGCTGTGAAGTTTGTGACATGCGCAAGGGGCGATGGCTTCTCTA 1080
QY 1081 CACACACTAGAGCCCTCATCCACGACATGACATCAATAGCCGTAATGATGAT 1140
DB 1081 CACACACTAGAGCCCTCATCCACGACATGACATCAATAGCCGTAATGATGAT 1140
QY 1141 GAGGACATGACTGCGCGAATTAAGCATGCTGATGATCAATTTCTTTCAATGTCTGT 1200
DB 1141 GAGGACATGACTGCGCGAATTAAGCATGCTGATGATCAATTTCTTTCAATGTCTGT 1200
QY 1201 CGCATGTATGACATCTGCTGGGTAGCCCCCGAAGCTCTGACAGAGAACCTGTAACACACA 1260
DB 1201 CGCATGTATGACATCTGCTGGGTAGCCCCCGAAGCTCTGACAGAGAACCTGTAACACACA 1260
QY 1261 AACAGAGCTCAGCAGACATGAGATTTTGGAGGCTTCTGTGGAACTGGTACAGG 1320
DB 1261 AACAGAGCTCAGCAGACATGAGATTTTGGAGGCTTCTGTGGAACTGGTACAGG 1320
QY 1321 GAGTACCTCTTGTGACCTCTCAATATGAGATTTGAAATGGAAGTGGCATTTGGAAGC 1380
DB 1321 GAGTACCTCTTGTGACCTCTCAATATGAGATTTGAAATGGAAGTGGCATTTGGAAGC 1380
QY 1381 CTTGGGCTTACCATCCACAGAGTATTTCCCTCATGTGTGTAGCTATGAAGATCTGC 1440
DB 1381 CTTGGGCTTACCATCCACAGAGTATTTCCCTCATGTGTGTAGCTATGAAGATCTGC 1440
QY 1441 ATGAATGAAGACCTGCAAGAGGACCAATTTGACATGATTTGCTTATCTTGAAG 1500
DB 1441 ATGAATGAAGACCTGCAAGAGGACCAATTTGACATGATTTGCTTATCTTGAAG 1500
QY 1501 ATGACAGCAAGTGAAGATCTGGAAGTCTTGTGCTGAATCTCAGAGGTGTGCGGACATG 1560
DB 1501 ATGACAGCAAGTGAAGATCTGGAAGTCTTGTGCTGAATCTCAGAGGTGTGCGGACATG 1560
QY 1561 TGGGGGAAATGACCTTCCCAAGAGAGGCTGTGTTGCTCCCGGCTCTCACTAT 1620
DB 1561 TGGGGGAAATGACCTTCCCAAGAGAGGCTGTGTTGCTCCCGGCTCTCACTAT 1620
QY 1621 GGTACTACCCAGCTGTGGGCTCATCCCTTCCCATCTCCATCACTGTGGCAAGAG 1680
DB 1621 GGTACTACCCAGCTGTGGGCTCATCCCTTCCCATCTCCATCACTGTGGCAAGAG 1680
QY 1681 GCGGGGCTCAGAGCTTTTCACTTGCATGCTGCTCCCAATGGAAGGAGATCAAGC 1740
DB 1681 GCGGGGCTCAGAGCTTTTCACTTGCATGCTGCTCCCAATGGAAGGAGATCAAGC 1740
QY 1741 CCGCTGTCACTAATTAAGTTTATTAAGAAAAAATTAAGAAAAAATTAAGAAAAA 1789
DB 1741 CCGCTGTCACTAATTAAGTTTATTAAGAAAAAATTAAGAAAAAATTAAGAAAAA 1789
```

RESULT 3

RESOUR 3
US-09-390-425-1

US-09-390-423-1
: Sequence 1. Application US/09390425

; Patent No. 6338958

; FACILE NO. 6338938
; GENERAL INFORMATION:

; GENERAL INFORMATION:
: APPLICANT: Dedhar shoukar

APPLICANT: Hannigan, Shoukat

APPLICANT: HANNIGAN, GREG
TITLE OF INVENTION: INTERAXIN-LINKED KINASE AND ITS USES

TITLE OF INVENTION: LATENT
REFERENCE: KIN CON

FILE REFERENCE: KIN-2CON
CURRENT APPLICATION NUMBER: IIS/08/200 12E

CURRENT APPLICATION NUMBER: US/

; CURRENT FILING DATE: 1999-09-03
 ; EARLIER APPLICATION NUMBER: US00/000 024

EARLIER APPLICATION NUMBER: US661005123

EARLIER FILING DATE: 1995-12-21

; EARLIER APPLICATION NUMBER: US0

EARLIER FILING DATE: 1998

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: F

; SEQ ID NO 1

; LENGTH: 17

; TYPE: DNA

; ORGANISM: H. sapien

; FEATURE:

NAME/KEY: CDS

LOCATION: (157) .

NAME/KEY: Other

LOCATION: (

Query Match 100.0%; Score 1789; DB 4; Length 1789;

Best Local Similarity 100.0%; pred. No. 0;

Best local similarity 100.00, rscd: no: 0,
Matches 1789: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

1	QY	GAATTCACTCTCGACTGCTTACCACGGAGTTCCTCCCGGAGNAGATCCTCGACGCCGAGT	60
1	Db	GAATTCACTCTGTCGACTGCTACCACGGAGTTCCTCCCGGAGNAGATCCTCGACGCCGAGT	60
61	QY	CCCGAGGATAAAGCTTGGGGTTTCATCTCTCTTCCCTGGATCACTCCACAGTCCCTCAGGCT	120
61	Db	CCCGAGGATAAAGCTTGGGGTTTCATCTCTCTTCCCTGGATCACTCCACAGTCCCTCAGGCT	120
121	QY	TCCCCAATCAGGGGACTCGCGCCGGGACGCTGCTATGAGACGACATTTTTCACCTCAGTGC	180
121	Db	TCCCCAATCAGGGGACTCGCGCCGGGACGCTGCTATGAGACGACATTTTTCACCTCAGTGC	180
181	QY	CGGAGGGCAACGACAGTCGCGTTCGCTCGGCTGACACACGGAGAGACGACCTCAAC	240
181	Db	CGGAGGGCAACGACAGTCGCGTTCGCTCGGCTGACACACGGAGAGACGACCTCAAC	240
241	QY	CAGGGGACGATCATGCTTCTCCCCCTTGCACTGGGCCTGCCAGAGGGCCGCTCTGCT	300
241	Db	CAGGGGACGATCATGCTTCTCCCCCTTGCACTGGGCCTGCCAGAGGGCCGCTCTGCT	300
301	QY	GTGTTTGAGATGTTGATCATCGGGGGGCA CGGATCAATGTAATGAACCGTGGGGATGC	360
301	Db	GTGTTTGAGATGTTGATCATCGGGGGGCA CGGATCAATGTAATGAACCGTGGGGATGC	360
361	QY	ACCCCCCTGCATCTGGCAGCCAGTCATGGACACCGTGTATATTGTACAGAAGCTATTGCAG	420
361	Db	ACCCCCCTGCATCTGGCAGCCAGTCATGGACACCGTGTATATTGTACAGAAGCTATTGCAG	420
421	QY	TACAAGGCAGACATCAATGCAGTGAATGAACACGGGAATGTGCCCCCTGCACCTATGCCTGT	480
421	Db	TACAAGGCAGACATCAATGCAGTGAATGAACACGGGAATGTGCCCCCTGCACCTATGCCTGT	480
481	QY	TTTTTGGGGCCAAAGATCAAGTGGCAGAGGA CTTGTTGGCAAAATGGGGGCCCTTGT CAGCATC	540
481	Db	TTTTTGGGGCCAAAGATCAAGTGGCAGAGGA CTTGTTGGCAAAATGGGGGCCCTTGT CAGCATC	540
541	QY	TGTAAACAAGTATCGAGAGATGCCTGTGGACAAAGCCAAGGCACCCCTTGAGAGAGCTTCTC	600
541	Db	TGTAAACAAGTATCGAGAGATGCCTGTGGACAAAGCCAAGGCACCCCTTGAGAGAGCTTCTC	600
601	QY	CGAGAGCGGCGCAGAGAAGATGGGCCAAGATCTCAACCGTATTTCCATACAAGGACACATTC	660

Db 1681 GCGGGCTCAGAGCTTTGTCACTTGCACATGCTGTCTCCCAACATGGAGGATCAGCC 1740
Qy 1741 CCGCTGTCACTATAAGTTTATTTATGAAAAAAAAAAAAAAAAAAAA 1789
Db 1741 CCGCTGTCACTATAAGTTTATTTATGAAAAAAAAAAAAAAAAAAAA 1789

RESULT 4
US-09-566-906-1
; Sequence 1, Application US/09566906
; Patent No. 6369205
; GENERAL INFORMATION:
; APPLICANT: Dedhar, Shoukat
; APPLICANT: Hannigan, Greg
; TITLE OF INVENTION: Intergrin-Linked Kinase and its Uses
; FILE REFERENCE: KIN-2CON
; CURRENT APPLICATION NUMBER: US/09/566,906
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 09/390,425
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: US08/752,345
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1789
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (157)...(1512)
; NAME/KEY: Other
; LOCATION: (0)...(0)
US-09-566-906-1

Query Match 100.0%; Score 1789; DB 4; Length 1789;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1789; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCATCTGTGACGTGCTACACAGGAGTCCCGGAGAGATCTCGACGCCGAGT 60
Db 1 GAATTCATCTGTGACGTGCTACACAGGAGTCCCGGAGAGATCTCGACGCCGAGT 60
Qy 61 CCCGAGATTAAGCTTTGGGTTTATCTCTTCTCTGATCACTCAAGTCTTCAAGT 120
Db 61 CCCGAGATTAAGCTTTGGGTTTATCTCTTCTCTGATCACTCAAGTCTTCAAGT 120
Qy 121 TCCCAATCCAGGGAGCTCGGGCGGGGAGCTGCTATGAGAGATTTTCACTGAGTGC 180
Db 121 TCCCAATCCAGGGAGCTCGGGCGGGGAGCTGCTATGAGAGATTTTCACTGAGTGC 180
Qy 181 CCGGAGGAGCAACGAGTGCCTGCTGCTGCTGCTGCAACACGAGAGACGACTCAAC 240
Db 181 CCGGAGGAGCAACGAGTGCCTGCTGCTGCTGCTGCAACACGAGAGACGACTCAAC 240
Qy 241 CAGGGGAGCATGATGCTTCTTCTTCTTCTGCACTGGGCTGCGAGGGCCGCTCTGT 300
Db 241 CAGGGGAGCATGATGCTTCTTCTTCTTCTGCACTGGGCTGCGAGGGCCGCTCTGT 300
Qy 301 GTGGTTGAGATGTTGATCATGCGGGGGGAGCGGATCAATGTAATGAACCGTGGGATGAC 360
Db 301 GTGGTTGAGATGTTGATCATGCGGGGGGAGCGGATCAATGTAATGAACCGTGGGATGAC 360
Qy 361 ACCCCCTGATCTTGGACGCGAGTGCATGACACCGTGATTTGTACAGAGCTATTGGAG 420
Db 361 ACCCCCTGATCTTGGACGCGAGTGCATGACACCGTGATTTGTACAGAGCTATTGGAG 420
Qy 421 TACAGGAGAGATCAATGCACTGATGATGAACACGGGAATGTGCCCTGCACTATCTGT 480
Db 421 TACAGGAGAGATCAATGCACTGATGATGAACACGGGAATGTGCCCTGCACTATCTGT 480
Qy 481 TTTTGGGGCAAGATCAAGTGGCAGAGGAGCTGTGGCAATGGGGCCCTGTGACATC 540
Db 481 TTTTGGGGCAAGATCAAGTGGCAGAGGAGCTGTGGCAATGGGGCCCTGTGACATC 540

Db 481 TTTTGGGGCAAGATCAAGTGGCAGAGGAGCTGTGGCAATGGGGCCCTGTGACATC 540
Qy 541 TGTAAAGATATGAGAGATGCTCTGTGACAAAGCCAAAGGACACCTCTAGAGAGTTCTC 600
Db 541 TGTAAAGATATGAGAGATGCTCTGTGACAAAGCCAAAGGACACCTCTAGAGAGTTCTC 600
Qy 601 CGAGAGCGGGGAGAGATGGGGCAGAACTCAACCGTATTTCTATACAGAGACATTC 660
Db 601 CGAGAGCGGGGAGAGATGGGGCAGAACTCAACCGTATTTCTATACAGAGACATTC 660
Qy 661 TGAAGGGGAGCACCCGACTCGGCCCGGAATGGAACCTTGAAACAACTCTGGCAT 720
Db 661 TGAAGGGGAGCACCCGACTCGGCCCGGAATGGAACCTTGAAACAACTCTGGCAT 720
Qy 721 GACTTCAACAGCTTAATCTTCTGCAAGCTCAACGAAATCACTCTGAGAGCTATGG 780
Db 721 GACTTCAACAGCTTAATCTTCTGCAAGCTCAACGAAATCACTCTGAGAGCTATGG 780
Qy 781 AAGGGCGCTGGCAGGGGCAATGACATTTGTGGAAGGTGGAAGGTTGAGACTGAGT 840
Db 781 AAGGGCGCTGGCAGGGGCAATGACATTTGTGGAAGGTGGAAGGTTGAGACTGAGT 840
Qy 841 ACAAGGAAGACAGGAGCTTCAATGAAGAGTGTCCCGCTCAGGATTTTCTCGCATCA 900
Db 841 ACAAGGAAGACAGGAGCTTCAATGAAGAGTGTCCCGCTCAGGATTTTCTCGCATCA 900
Qy 901 AATGTCTCCAGTGTCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 901 AATGTCTCCAGTGTCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Qy 961 ACACCTGAGAGCGGTATGATATCCCTCAACATGACTCAATGAAGGACCAATTTGCTC 1020
Db 961 ACACCTGAGAGCGGTATGATATCCCTCAACATGACTCAATGAAGGACCAATTTGCTC 1020
Qy 1021 GTGACACAGAGCGGTGTGAAGTTTCTTGTGACATGAGGAGGAGGAGGAGGAGGAG 1080
Db 1021 GTGACACAGAGCGGTGTGAAGTTTCTTGTGACATGAGGAGGAGGAGGAGGAGGAG 1080
Qy 1081 CACACACTAGAGCGGCTCATCCACGACATCACTCAATAGCCGTAATGATGAT 1140
Db 1081 CACACACTAGAGCGGCTCATCCACGACATCACTCAATAGCCGTAATGATGAT 1140
Qy 1141 GAGGACATGACTGCGGCAATTAAGCAATGCTGATGATGATGATGATGATGATGAT 1200
Db 1141 GAGGACATGACTGCGGCAATTAAGCAATGCTGATGATGATGATGATGATGATGAT 1200
Qy 1201 CGCATGTATGACCTGCTGGGTAGCCCCGAAAGCTTCGAGAAAGCTGTAAGACA 1260
Db 1201 CGCATGTATGACCTGCTGGGTAGCCCCGAAAGCTTCGAGAAAGCTGTAAGACA 1260
Qy 1261 AACAGACGCTCAGCAGATGTGAGTTTGTGAGTCTTGTGGAACTGGTGAACGG 1320
Db 1261 AACAGACGCTCAGCAGATGTGAGTTTGTGAGTCTTGTGGAACTGGTGAACGG 1320
Qy 1321 GAGGTACCTTTTGTGACCTCTCCAAATATGAGATGGAATGAAGTGGCATTTGAAGC 1380
Db 1321 GAGGTACCTTTTGTGACCTCTCCAAATATGAGATGGAATGAAGTGGCATTTGAAGC 1380
Qy 1381 CTTGGGCTTACCATCCACAGATTTTCCCTCATGCTGTGATGAGTCTGATGAGTCTGC 1440
Db 1381 CTTGGGCTTACCATCCACAGATTTTCCCTCATGCTGTGATGAGTCTGATGAGTCTGC 1440
Qy 1441 ATGAATGAAGACCTGCAAGACGAAATTTGACATGATTTGCTTATCTTGAAG 1500
Db 1441 ATGAATGAAGACCTGCAAGACGAAATTTGACATGATTTGCTTATCTTGAAG 1500
Qy 1501 ATGCAAGCAAGTGAAGATGGAAGTCTTCTGAAATCCAGAGCTTCGGGACATGT 1560
Db 1501 ATGCAAGCAAGTGAAGATGGAAGTCTTCTGAAATCCAGAGCTTCGGGACATGT 1560
Qy 1561 TGGGGGAATGACCTCCCAAGACAGAGGCTCTGTTGGTCTCCCGGCTCCAGTAT 1620
Db 1561 TGGGGGAATGACCTCCCAAGACAGAGGCTCTGTTGGTCTCCCGGCTCCAGTAT 1620

QY 1621 GGTAACACCCAGCCGTTGCTCATCCCTTCCCTCCCTACCACTGTGGCAAGAG 1680
 DB 1621 GGTAACACCCAGCCGTTGCTCATCCCTTCCCTCCCTACCACTGTGGCAAGAG 1680
 QY 1681 GCGGAGCTCAGAGCTTTGTCACTTGCACATGCTGTCCCAACATGGAGGATCAGCC 1740
 DB 1681 GCGGAGCTCAGAGCTTTGTCACTTGCACATGCTGTCCCAACATGGAGGATCAGCC 1740
 QY 1741 CCGCTGTACAAATAGTTATTTATGAAAAA 1789
 DB 1741 CCGCTGTACAAATAGTTATTTATGAAAAA 1789

RESULT 6

US-09-016-434-1071
 ; Sequence 1071, Application US/09016434
 ; Patent No. 6500938
 ; GENERAL INFORMATION:
 ; APPLICANT: Janice Au-Young
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 ; NUMBER OF SEQUENCES: 1490
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,434
 ; FILING DATE: HERewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0002 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1071:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1786 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GENBANK
 ; CLONE: G1146128
 ; US-09-016-434-1071

Query Match 99.0%; Score 1771.4; DB 4; Length 1786;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1785; Conservative 0; Mismatches 1; Indels 3; Gaps 1;
 QY 1 GAATTCATGTGCACTGCTACACGAGGATCCCGGAGAGGATCCCTGACCCGAGT 60
 DB 1 GAATTCATGTGCACTGCTACACGAGGATCCCGGAGAGGATCCCTGACCCGAGT 60
 QY 61 CCGGAGATGAAGCTTGGGATTCATCTCTCCCTGATCACTCAGTCTCAGGCT 120
 DB 61 CCGGAGATGAAGCTTGGGATTCATCTCTCCCTGATCACTCAGTCTCAGGCT 120

QY 121 TCCCAATCCAGGGGACTCGGGCCCGGAGACGCTGCTATGAGACGACATTTTCACTCAGTGC 180
 DB 121 TCCCAATCCAGGGGACTCGGGCCCGGAGACGCTGCTATGAGACGACATTTTCACTCAGTGC 180
 QY 181 CCGGAGGCGCAACGAGTCCGCTTCCCTGTGCTGCAACAACCGAGAGACGACCTCAAC 240
 DB 181 CCGGAGGCGCAACGAGTCCGCTTCCCTGTGCTGCAACAACCGAGAGACGACCTCAAC 240
 QY 241 CAGGGGAGACGATCATGCTTCTCCCTTTCGACTGCGGCTTCCGAGAGGCGCTCTGCT 300
 DB 241 CAGGGGAGACGATCATGCTTCTCCCTTTCGACTGCGGCTTCCGAGAGGCGCTCTGCT 300
 QY 301 GTGGTTGATGTTGATCATGCGGGGGGCAAGGATCAATGATATGACCGTGGGATGAC 360
 DB 301 GTGGTTGATGTTGATCATGCGGGGGGCAAGGATCAATGATATGACCGTGGGATGAC 360
 QY 361 ACCCCCTGCATCTGGCAGCAGTATGAGACACCTGATATTGTACAGAGCTATTGAG 420
 DB 361 ACCCCCTGCATCTGGCAGCAGTATGAGACACCTGATATTGTACAGAGCTATTGAG 420
 QY 421 TACAAGCAGACATCATATGACGTGAATGAACAAGGAAATGTCCTTCGACTATGCTGT 480
 DB 421 TACAAGCAGACATCATATGACGTGAATGAACAAGGAAATGTCCTTCGACTATGCTGT 480
 QY 481 TTTTGGGGCCCAAGATCAAGTGGCAGAGACCTGTGGAATATGGGGCCCTTGTCAAGCATC 540
 DB 481 TTTTGGGGCCCAAGATCAAGTGGCAGAGACCTGTGGAATATGGGGCCCTTGTCAAGCATC 540
 QY 541 TGTAACTAGTATGAGAGATGCTGTGGAACAAGCCAGGACCCCTGAGAGCTTCTC 600
 DB 541 TGTAACTAGTATGAGAGATGCTGTGGAACAAGCCAGGACCCCTGAGAGCTTCTC 600
 QY 601 CGAGAGCGGGGAGAGAGATGGGCCAGATCTCAACCGTATTCATACAGAGACATTC 660
 DB 601 CGAGAGCGGGGAGAGAGATGGGCCAGATCTCAACCGTATTCATACAGAGACATTC 660
 QY 661 TGGAGGGGACACCCCGACTCGGGCCGGAATGGAACCTGGAACAAACACTCTGGCAT 720
 DB 661 TGGAGGGGACACCCCGACTCGGGCCGGAATGGAACCTGGAACAAACACTCTGGCAT 720
 QY 721 GACTTCAACAGCTTAACTTCTGAGAGCTCAACGAGAACTCTGAGAGCTATAG 780
 DB 721 GACTTCAACAGCTTAACTTCTGAGAGCTCAACGAGAACTCTGAGAGCTATAG 780
 QY 781 AAGGCGCTGCGAGGCAATGACATTTGCTGAAGGTGCTGAAGTTTGAAGCTGAGT 840
 DB 781 AAGGCGCTGCGAGGCAATGACATTTGCTGAAGGTGCTGAAGTTTGAAGCTGAGT 840
 QY 841 ACAAGGAAGAGCAGGAGATCTCAATGAAGAGTGTCCCGGCTCAGGATTTTCTCGATCCA 900
 DB 841 ACAAGGAAGAGCAGGAGATCTCAATGAAGAGTGTCCCGGCTCAGGATTTTCTCGATCCA 900
 QY 901 AATGTCCTCCAGTGTGAGTGTGCTGCGAGTCTCACTGCTCTCATCTTCACTTCAATC 960
 DB 901 AATGTCCTCCAGTGTGAGTGTGCTGCGAGTCTCACTGCTCTCATCTTCACTTCAATC 960
 QY 961 ACACATGATGCGGTATGATTCCTTACATGATGATGATGAGGACCAATTTGCTC 1020
 DB 961 ACACATGATGCGGTATGATTCCTTACATGATGATGATGAGGACCAATTTGCTC 1020
 QY 1021 GTGACCCAGAGCAGGCTGTGAAGTTTCTTTCGACATGCGAAGGGGATGCTCTCTTA 1080
 DB 1021 GTGACCCAGAGCAGGCTGTGAAGTTTCTTTCGACATGCGAAGGGGATGCTCTCTTA 1080
 QY 1081 CACACACTAGAGCCCTCATCCACAGACATGACATCAATAGCCGATGATATGAT 1140
 DB 1081 CACACACTAGAGCCCTCATCCACAGACATGACATCAATAGCCGATGATATGAT 1140
 QY 1141 GAGGACATGACTGCGCAATTAGCATGAGCTGATGCAATTTCTTTTCAATGTCCTGCT 1200
 DB 1141 GAGGACATGACTGCGCAATTAGCATGAGCTGATGCAATTTCTTTTCAATGTCCTGCT 1200

Qy	1201	CGCATGTATGCACCTGCTCGGTAGCCCCCGAAGCTCTGCAGAAAGAGCTG	1260
Db	1201	CGCATGTATGCACCTGCTCGGTAGCCCCCGAAGCTCTGCAGAAAGAGCTG	1260
Qy	1261	AACAGAGCCTCAGCAGACATGTGGAGTTTTCAGTCTTCTGTGGGAACTG	1320
Db	1261	AACAGAGCCTCAGCAGACATGTGGAGTTTTCAGTCTTCTGTGGGAACTG	1320
Qy	1321	GAGTACCCCTTGTCTGACCTCTCCAATATGGAGATTGGAAATGAAGTGG	1380
Db	1321	GAGTACCCCTTGTCTGACCTCTCCAATATGGAGATTGGAAATGAAGTGG	1380
Qy	1381	CTTCGGCCTACCATCCCAACAGGTAATTCCTCCCTCATGTGTGAAGTCAT	1440
Db	1381	CTTCG---TACCATCCCAACAGGTAATTCCTCCCTCATGTGTGAAGTCAT	1437
Qy	1441	ATGAATGAAGACCCTGCAAGCCAGCACCAATTTTGACATGATCTGCCTAT	1500
Db	1438	ATGAATGAAGACCCTGCAAGCCAGCACCAATTTGACATGATCTGCCTAT	1497
Qy	1501	ATGCAGGACAAGTAGGACTGGAAAGTCCCTTGGCCCTGAACTCCAGAGGT	1560
Db	1498	ATGCAGGACAAGTAGGACTGGAAGTCCCTTGGCCCTGAACTCCAGAGGT	1557
Qy	1561	TGGGGGAATGCACCTCCCAAGAGCAGAGCCCTCTGGTTGCCTCCCGCCT	1620
Db	1558	TGGGGGAATGCACCTCCCAAGAGCAGAGCCCTCTGGTTGCCTCCCGCCT	1617
Qy	1621	GGTACTACCCAGCCTGGGGTCCATCCCTTCCCCCATCCCTACCACTGTG	1680
Db	1618	GGTACTACCCAGCCTGGGGTCCATCCCTTCCCCCATCCCTACCACTGTG	1677
Qy	1681	GGCGGGCTCAGAGCTTTGTCACTTGGCCACATGGTGTCTCCCAACATGG	1740
Db	1678	GGCGGGCTCAGAGCTTTGTCACTTGGCCACATGGTGTCTTCCAACATGG	1737
Qy	1741	CCGCCTGTCAATAAAGTTTATTTATGAAAAAATAAAAAAAAAAAAAA	1789
Db	1738	CCGCCTGTCAATAAAGTTTATTTATGAAAAAATAAAAAAAAAAAAAA	1786

RESULT 7

RESULT 7
 US-08/700-575-35
 ; Sequence 35, Application US/08700575
 ; Patent No. 581749
 ; GENERAL INFORMATION:
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Hawkins, Phillip R.
 ; APPLICANT: Wilde, Craig G.
 ; TITLE OF INVENTION: NOVEL HUMAN KINASE HOMOLOGS
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/700,575
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BILLINGS, LUCY J
 ; REGISTRATION NUMBER: 36749
 ; REFERENCE/DOCKET NUMBER: SP-100 US
 ; TELECOMMUNICATION INFORMATION:

Query Match 4.2%; Score 75.4; DB 4; Length 2894;
Best Local Similarity 52.4%; Pred. No. 2.2e-11;
Matches 166; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 269 TGCACGTGGCCCTGCGGAGGAGGCGCCCTGCTGTGTGAGATGTTGATCATCGGGGG 328
DB 439 TGCACGTGGCCACACATACATGAGGCGCACTTGATGTTGATGATGCTCATTAACATGCGG 498
QY 339 CACGATCATGATGATGAAACCGTGGGATGACACCCCGCTGATCTGGAGAGCATCATG 388
DB 499 CAGAAATGACCTGTAAAGGATTAAGAAAGGTTAAACCCCTGATCTGATGCTGAGCTTCAAG 558
QY 389 GACACCGTATATGATGACAGAGCTATGACATGACAGACAGACATCAATGATGATG 448
DB 559 GACATATTAATGTTGATCAAGCATCTCTGACCTGGGGTGAAGATGATGAATCATG 618
QY 449 AACACGGAGATGCCCCCTGACATATGCTGTTTTGGGGCCCAAGATCAAGTGGAGAG 508
DB 619 TCTATGAAATACACGCGCTTCAATCGCTGCTACATGACAGATGCTGTGTTAAG 678
QY 509 ACCGTGTGCAATGGGCGCTTGTACATCTGTAAACAGATGAGAGATGCTGTG 568
DB 679 AGTTATGACTACGATGCTAACTGAACCAACCAATATGAGTTACCCCTTTGC 738
QY 569 ACAAGCCAGGACACC 585
DB 739 ATTTGCTGCTGCTCC 755

RESULT 9
US-09-172-977-2
; Sequence 2, Application US/09172977
; Patent No. 5989863
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: HUMAN ANKRYN FAMILY PROTEIN
; FILE REFERENCE: Pf-0615 US
; CURRENT APPLICATION NUMBER: US/09/172,977
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 1288
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1808075
US-09-172-977-2

Query Match 4.0%; Score 71.2; DB 2; Length 1288;
Best Local Similarity 48.3%; Pred. No. 2.3e-10;
Matches 199; Conservative 0; Mismatches 213; Indels 0; Gaps 0;

QY 226 GAGAACGACCTTAACCAAGGAGGAGATCATGCTTCTCCCTTGACCTGGGCTGGCGA 285
DB 690 GACAACTCTGTCAACAGCAGACGCGGCTTACCCCTCATCTGGGCTTCGCGC 749
QY 286 GAGGCGCGCTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 345
DB 750 TTTGAGAGATTAAGACCTTCTGCTTCTGCTGAGTGGGAGCGACCCCTCACATCTG 809
QY 346 AACCGTGGGATGACACCCCTGATCTGGAGCAGTCAATGATGATGATGATGATGATG 405
DB 810 GCAAAAGAGGAGAGAGGCGCTGTGCGGACAGACAGGCGGCTCAACAACATTTGG 869
QY 406 CAGAAAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 465
DB 870 GGGCTGCTGAGAGCGTGAAGTGAACATCTATGATGATGATGATGATGATGATGATG 929
QY 466 CTGCACTATGCTGTTTTGGGGCCCAAGTCAAGTGGAGAGACTGTGCAATGGG 525

DB 920 CTGCTGTACGCTGTGCGCGGAGACGTAAGATCGTTGAGGCGCTTGCGCCGAGGC 989
QY 526 GCCCTTGCACATCTGTAACAAAGTATGAGAGATGCTGTGAGACAAAGCCAGCACCC 585
DB 990 GCTGACCTTACACCGAAGCGAGCTCTGTACACCCCGAATGAGACTTGTGCGGCTG 1049
QY 586 CTGAGAGAGCTTCTCGAGAGCGGCGGAGAAAGATGCGCCGAATCTCAACC 637
DB 1050 GGATACCGAAAGTCAACAGGTATGAGAAACACATCTCAAGCTCTTCC 1101

RESULT 10
US-09-702-705-1406
; Sequence 1406, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvik, Tom
; APPLICANT: Carter, Derrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1406
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-1406

Query Match 3.4%; Score 61.6; DB 4; Length 486;
Best Local Similarity 49.7%; Pred. No. 7.5e-08;
Matches 157; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

QY 254 ATGCTTTTCCCCCTTGACCTGGGCTCCGAGAGGCGGCTGTGCTGTGATGATG 313
DB 166 ATGCTGTACTCCCTTACATTATGACGCTTCAAAAACAGCATGATGATGCTGTGATG 225
QY 314 TGATCATCGGGGGGACAGATCAATGATGATGATGATGATGATGATGATGATGATG 373
DB 226 TACTGAAAGGGGGGCTTAATCAGATGCTTAAGACCATTAAGAGCTTACAGCAATGCA 285
QY 374 TGGCAGCAGTATGACACCGTATGATGATGATGATGATGATGATGATGATGATGATG 433
DB 286 GGGCAGCAGCAAGGATTAATCAAGATGATGATGATGATGATGATGATGATGATGATG 345
QY 434 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 493
DB 346 CAATATCAAGACATGAGGATTAACCTCTTACATGAGCTGTATGATGATGATGATG 405
QY 494 ATCAAGTGAAGAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 553
DB 406 TGAAGAAAGAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 465
QY 554 GAGAGATGCTGTGGA 569
DB 466 AAAAGACACCCCTGCA 481

RESULT 11
US-09-736-457-1406
; Sequence 1406, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:

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; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Rettet, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, AiJun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736.457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1406
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-736-457-1406

Query Match          3.4%; Score 61.6; DB 4; Length 486;
Best Local Similarity 49.7%; Pred. No. 7.5e-08;
Matches 157; Conservative 0; Mismatches 159; Indels 0; Gaps 0

Qy 254 ATGCGTTCTCCCTTTCGACTGGCGCCTGCCGAGAGGGCGCTCTGCTGTGTTGAGATGT 313
      |||||
Db 166 ATGCGTGTACTCCCTTACATTATTCAGCGTTCCGAAAAACAGGCATGAGATCGTGTCAATGT 225
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Qy 314 TGATCATCGGGGGGCGCGGATCAATGTAATGAACCGTGGGGATGACACCCCTTGCATC 373
      |||||
Db 226 TACTGGAAGCGGGGGCTTAATCCAGATGCTAAGGACCATATGAGGCTACAGCAATGCACC 285

Qy 374 TGGCAGCGCAGTCATGGACACCGTGATATTGTACAGAAAGCTATTGCAGTACAAGGCAGACA 433
      |||||
Db 286 GGGCAGCAGCAAGGGTAACTTGAAGATGATTTCATATCTTCTGTACTACAAAGCATCCA 345

Qy 434 TCAATGCAGTGAATGAACACGGGAATGTGCCCTGCACATATGCCCTGTGTTTTGGGGCCAA 493
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Db 346 CAAACATCCAAAGACACTGAGGGTAACACTCTCTACACTTAGCCTGTGATGAGGAGAG 405

Qy 494 ATCAAGTGGCAGAGGACCTGGTGCAATATGGGGCCCTTGTTCAGCATCTGTAAACAAGTATG 553
      |||||
Db 406 TGGNAGAAGCAAACTGCTGGTGTCCCAAGGAGCAAGTATTATTACATTGAGATATAAGAG 465

Qy 554 GAGAGATGCCTGTGGA 569
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/196,387
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 09/095,225
; APPLICATION NUMBER: 09/095,225
; FILING DATE: June 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4134 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ; HYPOTHETICAL: NO
; US-09-196-387-1

Query Match 3.4%; Score 61.6; DB 3; Length 4134;
Best Local Similarity 51.1%; Pred. No. 2.3e-07;
Matches 145; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

Qy 189 CAACGCAGTCGCCGTTTCGGCTGTGGCTGGACACACGAGAGACGACTCAACCCAGGGGGA 248
    |||||
Db 2087 CAACCCGCTGCTGTTGTAGAGTACCTGCTACACACCGGTGCCGATGTCATGCCAAGA 2146
    |||||

Qy 249 CGATCATGGCTTCTCCCTTGTGCACTGGGCTGCCAGAGGGCCGCTCTGCTGTGTTGA 308
    |||||
Db 2147 CAAGGGTGGCTTGGTGCCCCCTTCATATGCTCTTCATATGACACATATGAGGTGGCTGA 2206
    |||||

Qy 309 GATGTTTCATCATCGGGGGGCACGGATCAATGTAATGAACCGTGGGGATGACACCCCT 368
    |||||
Db 2207 GCTTTTAGTAGCATGGGGCTTCTGTAATGTGGCGGACTTATGAAATTTTACCCCTCT 2266
    |||||

Qy 369 GCATCTGGCAGCCAGTCATGGACACCGCTGATATGTTACAGAAGCTATTGCAGTACAAGGC 428
    |||||
Db 2267 CCATGAAGCAGCAGCTAAGGAAGTATGAAATCTGCAAGCTCTTTTAAACATGGAGC 2326
    |||||

Qy 429 AGACATCAATGCAGTGAATGAACACCGGAATGTCCTTGCAC 472
    |||||
Db 2327 AGATCCAACATAAAAGAACAGAGATGGAATACACCTTTGGATT 2370
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RESULT 12	RESULT 13
US-09-196-387-1	US-09-841-835-1
; Sequence 1, Application US/09196387	; Sequence 1, Application US/09841835
; Patent No. 6277613	; Patent No. 6506587
; GENERAL INFORMATION:	; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia	; APPLICANT: de Lange, Titia
; APPLICANT: Smith, Susan	; APPLICANT: Smith, Susan
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS	; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; TITLE OF INVENTION: OF USE THEREOF	; TITLE OF INVENTION: OF USE THEREOF
; NUMBER OF SEQUENCES: 12	; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:	; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson	; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor	; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack	; CITY: Hackensack
; STATE: New Jersey	; STATE: New Jersey
; COUNTRY: USA	; COUNTRY: USA
; ZIP: 07601	; ZIP: 07601
; COMPUTER READABLE FORM:	; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk	; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible	; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS	; OPERATING SYSTEM: PC-DOS/MS-DOS
Version #1.30	Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4134 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-09-841-835-1

Query Match 3.4%; Score 61.6; DB 4; Length 4134;
Best Local Similarity 51.1%; Pred. No. 2.3e-07;
Matches 145; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

189 CAACGCACTGCGCCGCTTGCCTGTGCTGACACACGAGAGACGCTCAACAGGGGGA 248
2087 CAACGCGTGTCTGTGTAGACTACTGTACACACGCTGCGATGTCACCAAGA 2146
249 CGATCATGGCTTCTCCCTTGCCTGACGCGGAGGCGGCTGCTGTGTGA 308
2147 CAAGGTGGCTGTGGCCCTTCATATGCTGCTCATATGAGACATAGAGTGGCTGA 2206
309 GATCTGATCATGCGGGGGGCGACGATCATATGAAACCGTGGGAGTAGACACCCCT 368
2207 GCTTTAGTAAGGCAATGGGGCTTCTGTCAATGTGGCGGACTTATGAAATTTACCCCT 2266
369 GCATCTGGCAGCGCATCATGACACCGATATTTGACAGAGTATTCAGTACAGGC 428
2287 CCATAGACAGAGCTTAAGAGAAATGTAATTCGCAAGCTCTTTTAAACATGAGAC 2326
429 AGACATCATGCGATGAAAGACACGGAATGTGCCCTGCACT 472
2337 AGATCAACTAATAAAGAACAGAGATGAAATACCTTTGATT 2370
DB

RESULT 14
US-09-196-387-7
Sequence 7, Application US/09196387
Patent No. 6277613
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRP1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/196,387
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4491 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 6..2027
US-09-196-387-7

Query Match 3.4%; Score 61.6; DB 3; Length 4491;
Best Local Similarity 51.1%; Pred. No. 2.4e-07;
Matches 145; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

189 CAACGCACTGCGCCGCTTGCCTGTGCTGACACACGAGAGACGCTCAACAGGGGGA 248
2444 CAACGCGTGTCTGTGTAGACTACTCTACACACGAGTCCGATGTCACCAAGA 2503
249 CGATCATGGCTTCTCCCTTGCCTGACGCGGAGGCGGCTGCTGTGTGA 308
2504 CAAGGTGGCTGTGGCCCTTCATATGCTGCTCATATGACACTATGAGTGGCTGA 2563
309 GATCTGATCATGCGGGGGGCGACGATCATATGAAACCGTGGGAGTAGACACCCCT 368
2564 GCTTTAGTAAGGCAATGGGGCTTCTGTCAATGTGGCGGACTTATGAAATTTACCCCT 2623
369 GCATCTGGCAGCGCATCATGACACCGTATTTGTAAGAGACTATTCAGTACAGGC 428
2624 CCATAGACAGAGCTTAAGAGAAATGTAATTCGCAAGCTCTTTTAAACATGAGAC 2683
429 AGACATCATGCGATGAAAGACACGGAATGTGCCCTGCACT 472
2684 AGATCAACTAATAAAGAACAGAGATGAAATACCTTTGATT 2727
DB

RESULT 15
US-09-841-835-7
Sequence 7, Application US/09841835
Patent No. 6506587
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRP1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/841,835

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/196,387

AFFIDAVIT
 FILING DATE:

FILED DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-230 CIPI

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTIC

LENGTH: 4491 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

MOLECULE LIFE: NO
HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

NAME/KEY: CDS
LOCATION: 6..2027

US-09-841-835-7

Query Match 3.4%; Score 61.6; DB 4; Length 4491;

Query Match 5.4%; Score 01.0; SD 4;
Best Local Similarity 51.1%; Pred. No. 2.4e-07;

Local Similarity	Seq. No.	Indels	Gaps
Matches 145; Conservative	0; Mismatches 139;	Indels 0;	Gaps 0;

Qy	189	CAACGCGAGTCGGCGTTCGCTGTGGCTGGACAACACGGAGAACGACCTCAACCGAGGGGA	248
Db	2444	CAACCGCGTGTCTGTTGTAGAGTACCTCTACACCGGTGCCGATGTCCATGCCCAAGA	2503

2444 CAACCGCGTCTGTTGTAGAGTACCTGCTACACCACGGTGCCGATGTCCATGCCAAGA 2503

QY 249 CGATCATGGCTTCTCCCCCTTGCACTGGGCCCTGCCGAGAGGGCCGCTCTGCTGTGGTTGA 308

Db 2504 CAAGGTGGCTTGGTGCCCTTCATAATGCCCTGTTCATATGGACACTATGAGGTGGCTGA 2563

309 GATGTTGATCATCGGGGGCACGGATCAATGTAATGAACCGTGGGATGACACCCCT 368

Db 2564 GCTTTTAGGCA TGGGGCTTCTGTCAATGTGGCGGACTTATGGAAATTTACCCCTCT 2623

QY 369 GCATCTGGCAGCCAGTCATGGACACCCGTGATATTGTACAGAGCTATTGCAGTACAAGGC 428

D**b** 2624 CCATGAAGCAGCAGCTAAAGGAAAGTATGAAATCTGCAAGCTCCTTTTAAACATGGAGC 2683

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Db 2684 AGATCCAACTAAAAAGAACAGAGATGGAAATACACCTTTGGATT 2727

Search completed: September 22, 2003, 19:14:09

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search completed:
Job time : 99 secs
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1	1789	100.0	1789	10	US-09-840-702-1
2	1352.6	75.6	1607	9	US-09-925-3032-336
3	610	34.1	1013	12	US-09-814-953-10253
4	437.4	24.4	484	11	US-09-918-995-15133
5	437.6	23.9	464	11	US-09-918-995-23944
6	328.4	18.4	330	9	US-09-922-217-435
7	328.4	18.4	330	10	US-09-833-263-435
8	328.4	18.4	330	13	US-10-025-880-435
9	240.8	13.5	568	14	US-10-106-698-2638
10	170.2	9.5	506	12	US-09-814-353-14739
11	127.8	7.1	301	10	US-09-917-8004-187
12	123.2	6.9	462	12	US-09-814-353-8305
13	123.2	6.9	462	12	US-09-814-353-8355
14	89	5.0	197	10	US-09-783-590-2528
15	86.6	4.8	370	11	US-09-918-995-8469
16	75.6	4.2	2355	14	US-10-164-080-6

17	75.4	4.2	2894	14	US-10-037-270-95	Sequence 95, Appl
18	72.4	4.0	3860	12	US-10-354-358-37	Sequence 37, Appl
19	71.2	4.0	1345	10	US-09-840-243B-10	Sequence 10, Appl
20	70	3.9	459	11	US-09-918-995-19815	Sequence 19815, A
21	67.4	3.8	2356	14	US-10-146-473-19	Sequence 19, Appl
22	64.4	3.6	572	14	US-10-198-846-9943	Sequence 9943, Ap
23	64.2	3.6	1002	12	US-10-204-456-1	Sequence 1, Appl
24	64.2	3.6	1158	9	US-09-860-192-48	Sequence 48, Appl
25	64.2	3.6	1158	10	US-09-758-593A-2	Sequence 2, Appl
26	64.2	3.6	1158	14	US-10-328-704-2	Sequence 2, Appl
27	63.8	3.6	569	10	US-09-758-593A-5	Sequence 5, Appl
28	63.8	3.6	569	14	US-10-328-704-5	Sequence 5, Appl
29	63	3.5	3286	10	US-09-504-389-1	Sequence 1, Appl
30	62.4	3.5	519	10	US-09-833-381-60	Sequence 60, Appl
31	62.2	3.5	6207	12	US-10-205-194-11	Sequence 118, Appl
32	61.6	3.4	486	10	US-09-736-457-1406	Sequence 1406, Ap
33	61.6	3.4	486	10	US-09-902-941-1406	Sequence 1406, Ap
34	61.6	3.4	486	10	US-09-849-626-1406	Sequence 1406, Ap
35	61.6	3.4	486	12	US-10-113-872-1406	Sequence 1406, Ap
36	61.6	3.4	486	14	US-10-017-754-1406	Sequence 1406, Ap
37	61.6	3.4	4134	9	US-09-841-835-1	Sequence 1, Appl
38	61.6	3.4	4134	11	US-09-972-1158-7	Sequence 7, Appl
39	61.6	3.4	4491	9	US-09-841-835-7	Sequence 7, Appl
40	61.6	3.4	4657	9	US-09-841-835-9	Sequence 9, Appl
41	61	3.4	1325	14	US-10-084-817-217	Sequence 217, App
42	61	3.4	1889	10	US-09-974-298-182	Sequence 182, App
43	61	3.4	1889	12	US-10-240-965-158	Sequence 158, App
44	60	3.4	4613	12	US-09-908-975-1406	Sequence 14906, A
45	60	3.4	4613	14	US-10-171-581-303	Sequence 303, App

ALIGNMENTS

RESULT 1

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? Sequence 1, Application US/09840704
? Patent No. US20020122801A1
? GENERAL INFORMATION:
? APPLICANT: Dechkar, Shoukat
? APPLICANT: Hannigan, Greg
? TITLE OF INVENTION: Intergrin-linked kinase and its Uses
? FILE REFERENCE: KIN-2CON
? CURRENT APPLICATION NUMBER: US/09/840,704
? CURRENT FILING DATE: 2001-04-23
? PRIOR APPLICATION NUMBER: 09/566,906
? PRIOR FILING DATE: 2000-05-09
? PRIOR APPLICATION NUMBER: US08/752,345
? PRIOR FILING DATE: 1996-11-19
? NUMBER OF SEQ. ID NOS: 16
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 1
? LENGTH: 1789
? TYPE: DNA
? ORGANISM: H. sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (157)...(1512)
? NAME/KEY: Other
? LOCATION: (0)...(0)
? US-09-840-704-1

Query Match 100.0%; Score 1789; DB 10; Length 1789;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1789; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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QY	61 <td>CCCGAGAGTAAAGCTTGGGGTTCACTCTCTCCCTGGATCACTCAACAGTCTCAGGCT <td>120</td> </td>	CCCGAGAGTAAAGCTTGGGGTTCACTCTCTCCCTGGATCACTCAACAGTCTCAGGCT <td>120</td>	120
Db	61 <td>CCCGAGAGTAAAGCTTGGGGTTCACTCTCTCCCTGGATCACTCAACAGTCTCAGGCT <td>120</td> </td>	CCCGAGAGTAAAGCTTGGGGTTCACTCTCTCCCTGGATCACTCAACAGTCTCAGGCT <td>120</td>	120

QY 121 TCCCAATCCAGGGGACTCGGCGCGGACGCTGCTATGGACGACATTTTCACTCAGTGC 180
Db 121 TCCCAATCCAGGGGACTCGGCGCGGACGCTGCTATGGACGACATTTTCACTCAGTGC 180
QY 181 CGGAGGGCAACGAGTGCCTGCTCGCTGCTGGCTGGCAACACGAGAAAGACCTCAAC 240
Db 181 CGGAGGGCAACGAGTGCCTGCTCGCTGCTGGCTGGCAACACGAGAAAGACCTCAAC 240
QY 241 CAGGGGACGATCATATGCTTCTCCCTTGGCTGCTGAGGCTCGGAGAGGGCGCTCTGCT 300
Db 241 CAGGGGACGATCATATGCTTCTCCCTTGGCTGCTGAGGCTCGGAGAGGGCGCTCTGCT 300
QY 301 GTGTTGAGATGTTGATCATCGGGGGGACGAGTCAATGTAATGAACCGTGGGATGAC 360
Db 301 GTGTTGAGATGTTGATCATCGGGGGGACGAGTCAATGTAATGAACCGTGGGATGAC 360
QY 361 ACCCCCTGTCATCTGGCAGCCAGTCAATGACACCGTGTATTTGACAGAAGCTATTGCG 420
Db 361 ACCCCCTGTCATCTGGCAGCCAGTCAATGACACCGTGTATTTGACAGAAGCTATTGCG 420
QY 421 TACAAGGACACATCAATGAGTGAATGAACACGAGGATGTGCCCTGCACATATGCCGTGT 480
Db 421 TACAAGGACACATCAATGAGTGAATGAACACGAGGATGTGCCCTGCACATATGCCGTGT 480
QY 481 TTTTGGGGCCCAAGATCAAGTGGCAGGACCTGGTGGCAATGGGGCCCTTGTGAGCATC 540
Db 481 TTTTGGGGCCCAAGATCAAGTGGCAGGACCTGGTGGCAATGGGGCCCTTGTGAGCATC 540
QY 541 TGTAAAGTATGGAGAGATCCTGTGGCAAAAGCCAAAGGACCCCTCGAGAGAGCTTCTC 600
Db 541 TGTAAAGTATGGAGAGATCCTGTGGCAAAAGCCAAAGGACCCCTCGAGAGAGCTTCTC 600
QY 601 CGAGAGGGGACAGAGATGGGCGAGATCTCAACCGTATTCATCAAGAGACATTC 660
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QY 781 AAGGCCCTGCGCAGGCAATGACATTTCTGTAAGGTGCTGAAGGTTCGAGACTGGAGT 840
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QY 961 ACACACTGGATGCGGTATGGATCCCTCTACATGTACTACATGAAGGACCAATTTCTGTC 1020
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Db 1021 GTGACACAGAGCAGGCTGTGAAGTTTCTTGGACATGGCAAGGGGATGGCTTCTCTA 1080
QY 1081 CACACACTAGAGCCCTCATCCAGACATGCATCAATAGCCGTAGTGTAAATGATTGAT 1140
Db 1081 CACACACTAGAGCCCTCATCCAGACATGCATCAATAGCCGTAGTGTAAATGATTGAT 1140
QY 1141 GAGGACATGACTGCCCGAATTAGCATGGCTGATCAAGTTCTCTTTTCCAATGCTCTGTT 1200
Db 1141 GAGGACATGACTGCCCGAATTAGCATGGCTGATCAAGTTCTCTTTTCCAATGCTCTGTT 1200

QY 1201 CGCATGTATGACCTGCTGGTAGCCCGGAGCTCTGCAGAAAGAGCCCTGAAGACACA 1260
Db 1201 CGCATGTATGACCTGCTGGTAGCCCGGAGCTCTGCAGAAAGAGCCCTGAAGACACA 1260
QY 1261 AACAGACGCTCAGCAGACATGTGGAGTTTTCAGTGTCTTGTGGGAACTGGTGACACGG 1320
Db 1261 AACAGACGCTCAGCAGACATGTGGAGTTTTCAGTGTCTTGTGGGAACTGGTGACACGG 1320
QY 1321 GAGTACCTTTTGTGACCTCTCCAATATGGAGATTTGAATGAAGGTGGCATTTGAAGGC 1380
Db 1321 GAGTACCTTTTGTGACCTCTCCAATATGGAGATTTGAATGAAGGTGGCATTTGAAGGC 1380
QY 1381 CTTCCGCTTACCATCCCAACAGGATTTTCCCTCATGTGTGAAGCTCATGAAGATCTGC 1440
Db 1381 CTTCCGCTTACCATCCCAACAGGATTTTCCCTCATGTGTGAAGCTCATGAAGATCTGC 1440
QY 1441 ATGAATGAAGACCTGCAAGGACCCAAATTTTGCATGATTTGTGCCTATCTTTGAGAAG 1500
Db 1441 ATGAATGAAGACCTGCAAGGACCCAAATTTTGCATGATTTGTGCCTATCTTTGAGAAG 1500
QY 1501 ATGCAGACAGTAGGACTGGAAGTCTTGGTGGCTTGAAGTTCAGAGGTGTCCGGACATGGT 1560
Db 1501 ATGCAGACAGTAGGACTGGAAGTCTTGGTGGCTTGAAGTTCAGAGGTGTCCGGACATGGT 1560
QY 1561 TGGGGGAATGCACCTCCCAAGCAGAGGCTCTGGTGGCTTGAAGTTCAGAGGTGTCCGGACATGGT 1620
Db 1561 TGGGGGAATGCACCTCCCAAGCAGAGGCTCTGGTGGCTTGAAGTTCAGAGGTGTCCGGACATGGT 1620
QY 1621 GGTACTACCCAGCCTCGGGTTCATCCCTTCCCAATCCCTACCTGTGCGCAAGAGG 1680
Db 1621 GGTACTACCCAGCCTCGGGTTCATCCCTTCCCAATCCCTACCTGTGCGCAAGAGG 1680
QY 1681 GCGGGCTCAGAGCTTTGTACATTCGACATGGTGTCTCCCAATCCCAATGGAGGTATCAGCC 1740
Db 1681 GCGGGCTCAGAGCTTTGTACATTCGACATGGTGTCTCCCAATCCCAATGGAGGTATCAGCC 1740
QY 1741 CCGCTGTCACAATAAAGTTTATTAAGAAAAAAGAAAAAAGAAAAA 1789
Db 1741 CCGCTGTCACAATAAAGTTTATTAAGAAAAAAGAAAAAAGAAAAA 1789

RESULT 2

US-09-925-302-336
; Sequence 336, Application US/09925302
; Patent No. US2002004941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 336
; LENGTH: 1607
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1162)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1449)
; OTHER INFORMATION: n equals a,t,g, or c

Query Match 75.6%; Score 1352.6; DB 9; Length 1607;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1375; Conservative 2; Mismatches 2; Indels 3; Gaps 2;


```
QY 1183 TCTTCCAAATGTCCTGGTCGATGTATGCACTGCTGGTAGCCCCCGAAGCTCTGCAG 1242
Db 404 TCTTTCAAATGTCCTGGTCGATGTATGCACTGCTGGTAGCCCCCGAAGCTCTGCAG 463
QY 1243 AAGAAGCCTGAAGACACAAAAGAGCGCTCAGACAGATGTGGAGTTTTCAGTGTCTTG 1302
Db 464 AAGAAGCCTGAAGACACAAAAGAGCGCTCAGACAGATGTGGAGTTTTCAGTGTCTTG 523
QY 1303 TGGGAACCTGTGACACGGGAGGTACCTTTCTGCTGACCTCTCAATATGGAGATTGGAAATG 1362
Db 524 TGGGAACCTGTGACACGGGAGGTACCTTTCTGCTGACCTCTCAATATGGAGATTGGAAATG 583
QY 1363 AAGGTGGCAATTTGGAAGGCTTCGGGCTACCACTCCACCAGGTATTTCCCTCATGTGTGT 1422
Db 584 AAGGTGGCAATTTGGAAGGCTTCGGGCTACCACTCCACCAGGTATTTCCCTCATGTGTGT 643
QY 1423 AAGCTCATGAAGATCTGCATGAATGAAGACCTGTGAAGCGACCCAAATTTGACATGATT 1482
Db 644 AAGCTCATGAAGATCTGCATGAATGAAGACCTGTGAAGCGACCCAAATTTGACATGATT 703
QY 1483 GTGCTATCTCTTGAAGATCGAGACAAAGTAGGACTGGAAGGTCTTGCCTGAACCTCA 1542
Db 704 GTGCTATCTCTTGAAGATCGAGACAAAGTAGGACTGGAAGGTCTTGCCTGAACCTCA 763
QY 1543 GAGGTGTGCGGACATGTGTTGGGGAAATGCACCTCTCCCAAAGCAGCAGGCTCTGTTGCC 1602
Db 764 GAGGTGTGCGGACATGTGTTGGGGAAATGCACCTCTCCCAAAGCAGCAGGCTCTGTTGCC 823
QY 1603 TCCCCCGCTCCAGTCATGTACTACCCAGCC-TGGGGTCAATCCCTTCCCCCATCCC 1661
Db 824 TCCCCCGCTCCAGTCATGTACTACCCAGCCATGGGTCATCCCTTCCCCCATCCC 883
QY 1662 TACCACCTGTG--CGCAAGAGGGGGGCTCAGAGCTTTGTCACTTGCACATGTTGCTC 1719
Db 884 TACCACCTGTGCCCCCAAGAGGGGGGCTCAGAGCTTTGTCACTTGCACATGTTGCTC 943
QY 1720 CCAACATGGGAGGATCAGCCCGCTCTCAATAAAAGTTTAT 1763
Db 944 CCAACATGGGAGGATCAGCCCGCTCTCAATAAAAGTTTCT 987

RESULT 4
US-09-918-995-15193
; Sequence 15193, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15193
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)-(484)
; OTHER INFORMATION: n = A,T,C or G
Query Match 24.4%; Score 437.4; DB 11; Length 484;
Best Local Similarity 99.5%; Pred. No. 4.9e-127;
Matches 438; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 952 ACTCTCATCACACTGGATCGGATGGATCCCTCTCAATATGTACTACATGAAGGCACC 1011
Db 44 ACNCTCATCACACTGGATGCCATATGGATCCCTCTCAATATGTACTACATGAAGGCACC 103
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QY 1012 AATTTCTGTCGTGGACACAGCCAGCGTGTGAAGTTTCTTTGGACATGGCAAGGGCATG 1071
Db 104 AATTTCTGTCGTGGACACAGCCAGCGTGTGAAGTTTCTTTGGACATGGCAAGGGCATG 163
QY 1072 GCCTTCTTACACACACTAGAGCCCCCTCATCCACGACATGCACCTCAATAGCCGTAGTGT 1131
Db 164 GCCTTCTTACACACACTAGAGCCCCCTCATCCACGACATGCACCTCAATAGCCGTAGTGT 223
QY 1132 ATGATTGATGAGGACATGACTGCCCGAATTAGCATGCTGATGTCAAGTTCTCTTTCCAA 1191
Db 224 ATGATTGATGAGGACATGACTGCCCGAATTAGCATGCTGATGTCAAGTTCTCTTTCCAA 283
QY 1192 TGTCTCTGTGCTGATGATGACCTGCTGCTAGCCCTGCTGGTAGCCCCCGAAGCTCTGCA 1251
Db 284 TGTCTCTGTGCTGATGATGACCTGCTGCTGGTAGCCCCCGAAGCTCTGCAAGAGGCT 343
QY 1252 GAAGACACAAACAGACGCTCAGCAGACATGTGGAGTTTTCAGTGTCTTGTGGAACTG 1311
Db 344 GAAGACACAAACAGACGCTCAGCAGACATGTGGAGTTTTCAGTGTCTTGTGGAACTG 403
QY 1312 GTGACACGGGAGGTACCTTTGCTGACCTCTCCAAATATGAGATTGGAAATGAAGTGGCA 1371
Db 404 GTGACACGGGAGGTACCTTTGCTGACCTCTCCAAATATGAGATTGGAAATGAAGTGGCA 463
QY 1372 TTGGAAGGCTTTCGGCCCTAC 1391
Db 464 TTGGAAGGCTTTCGGCCCTAC 483

RESULT 5
US-09-918-995-23944
; Sequence 23944, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23944
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)-(464)
; OTHER INFORMATION: n = A,T,C or G
Query Match 23.9%; Score 427.6; DB 11; Length 464;
Best Local Similarity 99.1%; Pred. No. 5.9e-124;
Matches 430; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 704 ACAAACACTCTGGCATTGACTTTCAAACAGCTTAACTTCTGACGAGCTCAACGAGATC 763
Db 31 AGATACACTCTGGCATTGACTTTCAAACAGCTTAACTTCTGACGAGCTCAACGAGATC 90
QY 764 ACTCTGGAGAGCTATGGAAGGGCCGCTGGCAGGGCAATGACATTTGCTGAAGGTGCTGA 823
Db 91 ACTCTGGAGAGCTATGGAAGGGCCGCTGGCAGGGCAATGACATTTGCTGAAGGTGCTGA 150
QY 824 AGGTTCCGAGACTGGAGTACAGGAGAGCAGGAGCTTCAATGAAGAGTGTCCCGGCTCA 883
Db 151 AGGTTCCGAGACTGGAGTACAGGAGAGCAGGAGCTTCAATGAAGAGTGTCCCGGCTCA 210
QY 884 GGATTTTCTGCTATCCAAATGTGCTCCAGTGTAGGTGCTGCTGCTGCTGCTGCTGCTGCT 943
Db 211 GGATTTTCTGCTATCCAAATGTGCTCCAGTGTAGGTGCTGCTGCTGCTGCTGCTGCTGCT 270
QY 944 CTATCTCTCTCTCATCACACACTGGATGCGGTATGGATCCCTCTCAATATGTACTACATG 1003
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Db 271 CTCATCTACTCTCATCAACACAGTGGATGCCGTATGATCCCTCTACATGACTACATG 330
Qy 1004 AAGGACCAATTTCTCGGACCGAGCCAGGCTGTGAAGTTTCTTTGGACATGGCA 1063
Db 331 AAGGACCAATTTCTCGGACCGAGCCAGGCTGTGAAGTTTCTTTGGACATGGCA 390
Qy 1064 GGGGATGGCTTCTTACACACATAGAGCCCTATCCACGATGCACTCAATAGCC 1123
Db 391 GGGGATGGCTTCTTACACACATAGAGCCCTATCCACGATGCACTCAATAGCC 450
Qy 1124 GTAGTGAATGATT 1137
Db 451 GTAGTGAATGATT 464

RESULT 6
US-09-922-217-435/c
Sequence 435, Application US/09922217
Patent No. US20020076414A1
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tonglong
APPLICANT: Jiang, Yugu
APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 435
LENGTH: 330
TYPE: DNA
ORGANISM: Homo sapiens
US-09-922-217-435

Query Match 18.4%; Score 328.4; DB 9; Length 330;
Best Local Similarity 99.7%; Pred. No. 8.8e-93;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 996 ACTACATGAAGGACCAATTTCTGCTGAGACCAAGCCAGGCTGTGAAGTTTGGTGA 1055
Db 330 ACTACATGAAGGACCAATTTCTGCTGAGACCAAGCCAGGCTGTGAAGTTTGGTGA 271
Qy 1056 CATGCAAGGGGCAATGCTTCTCTACACACATAGAGCCCTATCCACGATGCACT 1115
Db 270 CATGCAAGGGGCAATGCTTCTCTACACACATAGAGCCCTATCCACGATGCACT 211
Qy 1116 CAATAGCCGTAGTGAATGATGATGAGACATGACTGCCCGCAATTAGCATGGTATGT 1175
Db 210 CAATAGCCGTAGTGAATGATGATGAGACATGACTGCCCGCAATTAGCATGGTATGT 151
Qy 1176 CAAGTTCTCTTCCAAATGCTCGTGCATGATGACATGCTGCTGGTGAAGCCCCGAAGC 1235
Db 150 CAAGTTCTCTTCCAAATGCTCGTGCATGATGACATGCTGCTGGTGAAGCCCCGAAGC 91
Qy 1236 TCTGCAAGAAAGCCTGAAGACACAAGAGCGCTCAGACGATGTGGAGTTTGGAGT 1295
Db 90 TCTGCAAGAAAGCCTGAAGACACAAGAGCGCTCAGACGATGTGGAGTTTGGAGT 31
Qy 1296 GCTTCTGTGGAACTGTGACACGGGAGGT 1325
Db 30 GCTTCTGTGGAACTGTGACACGGGAGGT 1

RESULT 7
US-09-833-263-435/c
Sequence 435, Application US/09833263
Patent No. US20020110547A1
GENERAL INFORMATION:
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolk, John A.
APPLICANT: Meagher, Madeleine J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C12
CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 435
LENGTH: 330
TYPE: DNA
ORGANISM: Homo sapiens
US-09-833-263-435

Query Match 18.4%; Score 328.4; DB 10; Length 330;
Best Local Similarity 99.7%; Pred. No. 8.8e-93;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 996 ACTACATGAAGGACCAATTTCTGCTGAGACCAAGCCAGGCTGTGAAGTTTGGTGA 1055
Db 330 ACTACATGAAGGACCAATTTCTGCTGAGACCAAGCCAGGCTGTGAAGTTTGGTGA 271
Qy 1056 CATGCAAGGGGCAATGCTTCTCTACACACATAGAGCCCTATCCACGATGCACT 1115
Db 270 CATGCAAGGGGCAATGCTTCTCTACACACATAGAGCCCTATCCACGATGCACT 211
Qy 1116 CAATAGCCGTAGTGAATGATGATGAGACATGACTGCCCGCAATTAGCATGGTATGT 1175
Db 210 CAATAGCCGTAGTGAATGATGATGAGACATGACTGCCCGCAATTAGCATGGTATGT 151
Qy 1176 CAAGTTCTCTTCCAAATGCTCGTGCATGATGACATGCTGCTGGTGAAGCCCCGAAGC 1235
Db 150 CAAGTTCTCTTCCAAATGCTCGTGCATGATGACATGCTGCTGGTGAAGCCCCGAAGC 91
Qy 1236 TCTGCAAGAAAGCCTGAAGACACAAGAGCGCTCAGACGATGTGGAGTTTGGAGT 1295
Db 90 TCTGCAAGAAAGCCTGAAGACACAAGAGCGCTCAGACGATGTGGAGTTTGGAGT 31
Qy 1296 GCTTCTGTGGAACTGTGACACGGGAGGT 1325
Db 30 GCTTCTGTGGAACTGTGACACGGGAGGT 1

RESULT 8
US-10-025-380-435/c
Sequence 435, Application US/10025380
Patent No. US20020182191A1
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tonglong
APPLICANT: Jiang, Yugu
APPLICANT: Smith, Carole L.
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Skelky, Yasir A. W.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedrick Thomas S.
APPLICANT: Carter, Darick

```

; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (429)..(429)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (444)..(444)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (455)..(455)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (457)..(457)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (508)..(508)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (524)..(524)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (526)..(526)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (555)..(555)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (557)..(557)
; OTHER INFORMATION: n equals a,t,g, or c
; US-10-106-698-2638

Query Match 13.5%; Score 240.8; DB 14; Length 568;
Best Local Similarity 97.2%; Pred. No. 4.6e-65;
Matches 245; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 451 CACGGAATGTGCCCTGCACACTGTCTTTTGGGGCCCAAGATCAAGTGGCAGAGGAC 510
Db 2 CACGGAATGTGCCCTGCACACTGTCTTTTGGGGCCCAAGATCAAGTGGCAGAGGAC 61
QY 511 CTGCTGGCAAAATGGGGCCCTTGTCAGCATCTGTAAACAAGTATGGAGAGATGCCTGTGGAC 570
Db 62 CTGCTGGCAAAATGGGGCCCTTGTCAGCATCTGTAAACAAGTATGGAGAGATGCCTGTGGAC 121
QY 571 AAGCCAAAGCACCCCTGAGAGAGCTTCTCCGAGAGCGGGCAGAGAAGATGGGCCCAAGAT 630
Db 122 AAGCCAAAGCACCCCTGAGAGAGCTTCTCCGAGAGCGGGCAGAGAAGATGGGCCCAAGAT 181
QY 631 CTCAACCGTATTCATACAGGACACATTCCTGAAGGGGACACCCGCACTCGGCCCGGA 690
Db 182 CTCAACCGTATTCATACAGGACACATTCCTGAAGGGGACACCCGCACTCGGCCCGGT 241
QY 691 AATGGAACCCCTG 702
Db 242 GAGTCACCACGTG 253

RESULT 10
US-09-814-353-14739
; Sequence 14739, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25

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PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14739
LENGTH: 506
TYPE: DNA
ORGANISM: Homo sapiens
US-09-814-353-14739

Query Match 9.5%; Score 170.2; DB 12; Length 506;
Best Local Similarity 98.3%; Pred. No. 7.5e-43;
Matches 172; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1123 CGTACTGTAATGATGAGACATGACTGCCGATTAGCATGCTGATGTCAAGTTC 1182
DB 332 CGTCGGTAATGATGAGACATGACTGCCGATTAGCATGCTGATGTCAAGTTC 391
QY 1183 TCTTCCATGCTCGTGCATGTATGACCTGCTGGGTAGCCCGAAGCTCTGCAG 1242
DB 392 TCTTCCATGCTCGTGCATGTATGACCTGCTGGGTAGCCCGAAGCTCTGCAG 451
QY 1243 AAGAAGCTGAAAGACAAAGAGAGCTGAGAGATGTGAGTTTGCAGTGC 1297
DB 452 AAGAAGCTGAAAGACAAAGAGAGCTGAGAGATGTGAGTTTGCAGTGC 506

RESULT 11

US-09-917-800A-187/C
Sequence 187, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Casle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: Patencin Ver. 2.1
SEQ ID NO 187
LENGTH: 301
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:

OTHER INFORMATION: Genbank Accession No. US20020119462A1 AAB66435
US-09-917-800A-187

Query Match 7.1%; Score 127.8; DB 10; Length 301;
Best Local Similarity 70.8%; Pred. No. 1.3e-29;
Matches 213; Conservative 0; Mismatches 82; Indels 6; Gaps 3;

QY 1493 TTGGAAGATGCAGACAAAGTAGAGCTGAAGCTCTGCGAATCCAGAGGTGG 1552
DB 301 TCGAAGATGCAGACAAAGTAGAGCTGAAGCTCTGCGAATCCAGAGGTGG 242
QY 1553 GACATGTTGGGGAATGACCTCCCAAGACAGAGCCTCTGCTGCTCCCGGCT 1612
DB 241 CATATGCTGACGAAATTAATTTCCCTGAAGTGAAGTTGTGCTGCTCCAGTCT 182
QY 1613 CCAGTATGTAATCAACCCAG-CTGGGGTCCATCCCTTCCCATCCTAACACTGT- 1670
DB 181 CTAATCGGTGTAATCAACCCAGACAGAGAGACTTCCCTGTCAATCAACACTGTA 122
QY 1671 -GCCAGAGGGGGGCTCAGAGCTTGTCACTTGCACATGGTGTCTCCCAAGAT 1726
DB 121 GCCCTGAGAGACATGGGACAGAGAGAGTCAAAATGCACATGATTCACAGACT 62
QY 1727 GGAAGGATCAAGCCCGCTGTCACATTAAGTTATTATGAAAAA 1786
DB 61 GGAAGGATCAAGCACTGCTGTAAATTAATTAAGTGA 2
QY 1787 A 1787
DB 1 A 1

RESULT 12

US-09-814-353-2009
Sequence 2009, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2009
LENGTH: 462
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 8
OTHER INFORMATION: n = A,T,C or G
US-09-814-353-2009

Query Match 6.9%; Score 123.2; DB 12; Length 462;
Best Local Similarity 97.7%; Pred. No. 4.6e-28;
Matches 125; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1123 CGTAGTGAATGATTGATGAGACATGACTGCCGAATTAGCATGGCTGATGTCAGGTTTC 1182
Db 335 CGTCGGGTAATGATTGATGAGACATGACTGCCGAATTAGCATGGCTGATGTCAGGTTTC 394
QY 1183 TCTTTCCAAATGCTCTGGTGGCATGTATGCACCTGCTGGTAGGCCCGAAGCTCTGCAG 1242
Db 395 TCTTTCCAAATGCTCTGGTGGCATGTATGCACCTGCTGGTAGGCCCGAAGCTCTGCAG 454
QY 1243 AAGAAGCC 1250
Db 455 AAGAAGCC 462

RESULT 13

US-09-814-353-8355
; Sequence 8355, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIORITY FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
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US-09-814-353-8355

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Db 395 TCTTTCCAAATGCTCTGGTGGCATGTATGCACCTGCTGGTAGGCCCGAAGCTCTGCAG 454
QY 1243 AAGAAGCC 1250
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RESULT 14

US-09-783-590-2528
; Sequence 2528, Application US/09783590
; Patent No. US20020110850A1

; GENERAL INFORMATION:

; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; PRIORITY FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
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US-09-783-590-2528

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REFERENCE
AUTHORS

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplexed capillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

REFERENCE
AUTHORS

4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Konno, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaïdo, I., Pesole, G., Quackenbush, J., Schrim, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldairelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bona, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Schonwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schombach, C., Seva, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
11217851

REFERENCE
AUTHORS

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1728)

REFERENCE
AUTHORS

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, K., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Direct Submission

REFERENCE
AUTHORS

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

COMMENT

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase

and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTTCTCAGTTAATTAATCCCCCCCCC 3'] cDNA was cleaved with XhoI and SclI. Cloning sites, 5' end: XhoI; 3' end: SclI.
Host: SOUR.

FEATURES
source

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Matches 1497; Conservative 0; Mismatches 168; Indels 4; Gaps 2;

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QY 342 AATGAACCGTGGGATGACACCCCTGTCATCTGCGAGCCAGTATGACACCGTGATAT 401
DB 299 GATGAATCGTGGGATGATACCCCTTGCACCTGGCAGCTAGTCATGACACCGTGACAT 358
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QY 462 GCCCTGCACTATGCTGTGTTTGGGGCCAAGATCAAGTGCAGAGGACCTGTTGGGAAA 521
DB 419 GCCATTCACATATGATGTTTCTGGGGCCAAGACCGAGTGCAGAGGACCTGTTGGCTAA 478
QY 522 TGGGGCCCTTCTGACGATCTCTAAACAGTATGGAGAGATGCTGTGGGACAAAGCCAAAGGC 581
DB 479 CGGGGCTTCTGTGAGCATCTGTACAGATATGGAGAGATGCTGTGGGACAAAGCCAAAGGC 538
QY 582 ACCCTGAGAGAGCTTCTCCGAGAGCGGGCAGAGAAGATGGGCCAGAAATCTCAACCGTAT 641
DB 539 ACCCTTAGAGAGCTTCTCCGAGAGCGGGCAGAGAAAATGGGCCAGAAATCTCAACCGTAT 598
QY 642 TCCATACAGAGACATCTCTGGAAGGGGACCAACCGGCACTCGGCCCGGAAATGGAACCT 701
DB 599 TCCATACAGAGACATCTCTGGAAGGGGACCACTCGCAACAGGGCCCCGAAATGGGACCT 658

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Db	659	GAACAAACACTCGGGTATTGACTTAAACAGCTCAACTTCTGGGCAAAAGCTCAAGAGA	718
OY	762	TCACTCTGAGAGCTATGAGAGGGCCGCTGGGACGGGCAATGACATTGTCGTGAAGTGT	821
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OY	822	GAAGTTTCGAGACTGAGATACAAAGAGAGCAGGAGCTTCAATGAAAGTGTCCCCGCT	881
Db	779	GAAGTTTCGAGACTGAGATACAAAGAGAGCAAGAGCTTCAATGAGAAATGTCCCCGCT	838
OY	882	CAGGATTTTCTGGCATCCAAATGTGCTCCAGTCTAGTGGCTGTGCACCTGC	941
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Db	1559	CTCCGCCCTCTCTATCATGTACTACCCAGTTATGGACCTTGTTCCTGTCTCCATCC	1611
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DEFINITION	Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610008x16 product:integrin linked kinase, full insert sequence.			
ACCESSION	AK002344			
VERSION	AK002344.1	GI:12832253		
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ORGANISM	Mus musculus			
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AUTHORS	1			
TITLE	Carninci, P. and Hayashizaki, Y.			
JOURNAL	High-efficiency full-length cDNA cloning			
MEDLINE	Meth. Enzymol. 303, 19-44 (1999)			
PUBMED	99279253			
REFERENCE	10349636			
AUTHORS	2			
TITLE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komuro, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
MEDLINE	Genome Res. 10 (10), 1617-1630 (2000)			
PUBMED	11042159			
REFERENCE	3			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagoka, S., Sasaki, N., Carninci, P., Komuro, H., Akiyama, U., Nishi, K., Kitanai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishite, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Keshiyagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.			
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format			
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)			
MEDLINE	20530913			
PUBMED	11076861			
REFERENCE	4			
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Komuro, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I., Saito, T., Okazaki, Y., Gotohori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Flatschmann, W., Gaasterland, T., Gissi, C., King, B., Kochwa, H., Kusui, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schiraldi, L.M., Staib, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Boujanga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hochman, M., Hume, D.A., Kamitani, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Sporch, K.F., Suzuki, H., Toyokawa, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohzuki, S. and Hayashizaki, Y.			
TITLE	Functional annotation of a full-length mouse cDNA collection			
JOURNAL	Nature 409 (6821), 685-690 (2001)			
MEDLINE	21085660			
PUBMED	11217851			
REFERENCE	5			
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.			
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs			
JOURNAL	Nature 420, 563-573 (2002)			
MEDLINE	6 (bases 1 to 1705)			
PUBMED	Adachi, J., Aizawa, K., Akahira, S., Akiyama, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,			

Furuno, M., Hanagaki, T., Hata, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]
 Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

COMMENT

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'-GAGAGAGAGCGCGCAACTCGAGTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGAGAGGATCCAGAGCTCAATTAAATTAACCCGCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.

FEATURES

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 QY 222 CACGAGAACGACCTCAACACGAGGGGACGATCATGGCTTCTCCCTTGCATGGGCTG 281
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 QY 159 CACAGAGAACGACCTCAATCAGGGGGATGATCATGGCTTCTCCCTTGCATGGGCTG 218
 DB |||||

QY 282 CCGAGAGGCGCGCTCTGCTGTGGTTGAGATGTTGATCATGCGGGGCGACCGATCAATGT 341
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 QY 342 AATGAACCGTGGGATGACACACCCCTGCTGATCTGGCAGCCAGTATGAGACACCGTGAT 401
 DB |||||
 QY 279 GATGAATCGTGGGATGATACCCCTGCTGACCTGGCAGCTAGTCTATGACACCGTGAT 338
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 QY 402 TGTACAGAGCTATTGCAAGTACAAGGACAGACATCAATGCACTGAATGAACACGGGAATGT 461
 DB |||||
 QY 339 TGTACAGAGCTATTGCAATACAAGGCTGACATCAATGCACTGAATGACACCGCAATGT 398
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 QY 462 GCCCTGCACTATGCTGTTTTCGGGCGCAAGATCAAGTGGCAGGACCTGTTGGCAAA 521
 DB |||||
 QY 399 GCCACTTTCACATGCAATGTTTCTGGGGCAAGACAGGTGGCAGAGGACCTTGGTGGCTAA 458
 DB |||||
 QY 522 TGGGCGCTTCTGACGATCTGTAACAAGTATGGAGAGATGCTGTGGACAAGCAAGGC 581
 DB |||||
 QY 459 CGGGCTTCTGAGCATCTGTAACAAGTATGGAGAGATGCTGTGGACAAGCAAGGC 518
 DB |||||
 QY 582 ACCCTGAGAGAGCTTCTCGAGAGCGGCGAGAGAAGATGGGCCAGAAATCTCAACCGTAT 641
 DB |||||
 QY 519 ACCCTTAGAGAGCTTCTCCGAGAACCGGCGAGAGAAATGGGCCAGAAATCTCAACCGTAT 578
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 QY 642 TCCATACAAGGACACATTTCTGGAAGGGGACCAACCGGACCTCGGCCCGGAAATGNAACCT 701
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 QY 579 TCCATACAAGGACACATTTCTGGAAGGGGACCACTCGCAAGGGCCCCGAAATGGGACCT 638
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 QY 702 GAACAAACACATCTCTGGCATTTGACTTTCAACACGCTTAACTTCTCGAGAGCTCAACAGAA 761
 DB |||||
 QY 639 GAACAAACACATCTCGGTTATGACTTTCAACACGCTCAACTTTCTGGCAAGCTCAATGAGAA 698
 DB |||||
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 DB |||||
 QY 699 TCATTCTGGAGAGCTTTGGAAAGGCGCTGCGAGGGCAATGATTTGTTGAAGGTGCT 758
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 QY 822 GAAGGTTTCGACATGGAGTACAAGGAGAGAGAGAGGAGCTTCAATGAAGAGTCTCCCGGCT 881
 DB |||||
 QY 759 GAAGGTTTCGACATGGAGTACAAGGAGAGAGAGGAGCTTCAATGAGGAAATGTCCCGGCT 818
 DB |||||
 QY 882 CAGGATTTTCTCGCATCCAAATGTGCTCCCAAGTGTAGGTGCTGCCAGCTCTCCACCTGC 941
 DB |||||
 QY 819 CAGGATTTTCTCACACCTTAACGTTCTCCAGTGTCTAGGTGCTTGGCAGGCTCCCCCAGC 878
 DB |||||
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 QY 879 CCCCCACCAACCTCATCACACATGATGATG- CATATGGATCTCTCTACAATGTCTACA 937
 DB |||||
 QY 1002 TGAAGGACCAATTTTCGTGCGGACCAAGAGCCAGGCTGTGAAGTTTGGTGGACATGCGC 1061
 DB |||||
 QY 938 TGAAGGACCAATTTTCGTGCGGACCAAGAGCCAGGCTGTGAAGTTTGGTGGACATGCGC 997
 DB |||||
 QY 1062 AAGGGGATGCGCTTCTCTACACACACTAGAGCCCTCATCCAGGACATGCACTCAATAG 1121
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 QY 1058 CCGAGTGTAAATGATGATGAAGATATGACTGCCCGGAATTCAGCATGGCTGATGTAAAGTT 1117
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 DB |||||
 QY 1178 GAAGAAGCCTGAAGACACAAACAGACGCTCAGCAGACATGTGGAGTTTTCGCGGTCTCT 1237
 DB |||||
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 DB |||||
 QY 1238 GTGGAACTGTGACACGGGAGGTGCCCTTGTGCTGACCTCTCTAATATGGAGATTGGAT 1297
 DB |||||

TITLE
JOURNAL

QY	1362	GAAAGTGGCATTTGMAAGGCTTTGGGCTTACCATCCACAGGATATTTCCCTCATGTGTG	1421
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Db	1356	TAACTCATGAAGATTTTGATGATGAAGACCTGCAAGAGCACCCAAGTTTGACATGAT	1415
QY	1482	TGTGCTTATCCTTGAAGAGATGACAGACAAAGTAGGACTGGACTGAACCTC	1541
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QY	1542	AGAGTGTGCGGACATGTGTTGGGGGAATGACACTCCCAAGACAGAGCTTGTTGTTC	1601
Db	1476	AGAAATGTTCAAACATGTGGCTGGGGAGTAGACTTTCTCCAAAGTTTAAAGACTCTGTGTTC	1535
QY	1602	CTCCCGCGCTCAGTCAATGGATACACCCAG-CTGGGGTTCATCCGCTTCCCCATCC	1666
Db	1536	CTCCCTGTCTTATTCATGTGACTAACCCAGTTATGGGACTTGTTCCTGCTCCATCC	1595
QY	1661	CTACCACTGT--GCGCAAGAGGGGCGGAGCTAGAGCTTGTGCACTTGCCACATGTTGTC	1717
Db	1596	CTACCACTGTAGCCCCCAAAAGGGGCTGAGAGCTTTGTGCACTTGCCACATGATGTC	1655
QY	1718	TCCCAACATGGAGAGGATCAGCCCCGCTGTACATATAAGTTTATATG	1767
Db	1656	TCCCAACATGGAGAGGATCAGCCCCGCTGTACATATAAGTTTATATG	1705

RESULT 3	AL579747/c	1201 bp	mRNA	linear	EST 01-JUN-2003
LOCUS	AL579747				
DEFINITION	Homo sapiens CDNA clone CSD0J003YK18 3-PRIME, mRNA sequence.				

ACCESSION AL579747 GI:31318027
 VERSION AL579747.2
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM	REFERENCE
Homio sapiens	1 (bases 1 to 1201)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
AUTHORS	Full-length cDNA libraries and normalization
TITLE	Unpublished
JOURNAL	On Feb 16, 2001 this sequence version replaced gi:12945092.
COMMENT	

Contact : Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 Evry cedex - France
Email : seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to more information cluster 6100.f For
more information about this cluster, see
[http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DJ003BF09NP1&cluster=6100.f](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DJ003BF09NP1&cluster=6100.f). Contact :
Peng Liang Email : liang@lifetech.com URL :
<http://fulllength.invitrogen.com/Invitrogen/Corporation/1600>
Faraday Avenue Genoscope sequence ID : CS0DJ003BF09NP1.

FEATURES	source	Location/Qualifiers
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		/clone_11b="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
		/note="1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 54.7%; Score 979.4; DB 9; Length 1201;
Best Local Similarity 92.8%; Pred.No. 2.6e-118;
Matches 1067; Conservative 30; Mismatches 44; Indels 9; Gaps 7;

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QY	629	ATCTCAACCGTATTTCCATACAGACACATTTCTGGAAGGGGACCACTCCGACTTGGCCCC	688
Db	1088	TATACMCCATATTTCCATATTAAGAAACATATYTGRRAGGGGMCCTCCCGACATCGSCCTC	1029
QY	689	GAATATGGAACCCCTGAACAAACACTCTGGACATATGCTTCAACACAGCTTAATCTCTGACGA	748
Db	1028	GAATATGGAACCCCTG-AACAAACAMTYTGCCATTTACTTCAACACAGCTTAATCTCTGACGA	970
QY	749	AGCTCAACGAGAAATCACTCTGAGAGCTATGGAAGGGGCGCTGCGA-GGGCAATGACATT	807
Db	969	AGCTCAACGAGAAATCACTCTGAGAGCTATGGAAGGGGCGCTGCGAAGGCAATGACATT	910
QY	808	GTCGTGAAGGTGCTGAAGGTTCCGAGACTGGAGTACAAAGAAAGACAGGACTTCAATGAA	867
Db	909	KTCGTGAAGGTGCTGAAGGTTCCGAGACTGGAGTACAAAGAAAGACAGGACTTCAATGAA	850
QY	868	GAGTGTCCCGGGCTCAGGATTTTTCGCATCTCAAAATGTGCTCCAGTGTAGAGTGGCTGC	927
Db	849	GAGTGTCCCGGGCTCAGGATTTTTCGCATCTCAAAATGTGCTCCAGTGTAGAGTGGCTGC	790
QY	928	CAGTGTCCACTGCTCCTCATCTCTCATCTATCACAACACTGAGTGGCTATGATCCCTC	987
Db	789	CAGTGTCCACTGCTCCTCATCTCTCATCTATCACAACACTGAGTGGCTATGATCCCTC	730
QY	988	TACATATGACTACATGGAAGGCAACCAATTTGCTGTGAGACCAAGCCAGGCTGTAACTTT	1047
Db	729	TACATATGACTACATGGAAGGCAACCAATTTGCTGTGAGACCAAGGCTGTAACTTT	670
QY	1048	GCTTTGGACATGCGAAGGGGCGATGGCTTCTCTACACACACTAGAGCCCTCATCCACGA	1107
Db	669	GCTTTGGACATGCGAAGGGGCGATGGCTTCTCTACACACACTAGAGCCCTCATCCACGA	610
QY	1108	CATGCACTCAATAGCCGTAATGTAATGATGATGATGATGATGATGATGATGATGATGATGATG	1167
Db	609	CATGCACTCAATAGCCGTAATGTAATGATGATGATGATGATGATGATGATGATGATGATGATG	550
QY	1168	GCTGATGCAAGTCTCTTTTCAATGTCTGGGTGCGATGTATGACACCTGCTGGGTGAGCC	1227
Db	549	GCTGATGCAAGTCTCTTTTCAATGTCTGGGTGCGATGTATGACACCTGCTGGGTGAGCC	490
QY	1228	CCCGAAGCTCTGCAGAAAGAGCCCTGGAAGACCAAAACAGACGCTCAGCAGACATGTGAGT	1287
Db	489	CCCGAAGCTCTGCAGAAAGAGCCCTGGAAGACCAAAACAGACGCTCAGCAGACATGTGAGT	430
QY	1288	TTTTCAGTGTCTCTGTGGGAACTGTGTACACAGGAGGTATCC-CTTTCTACCTCTCCAA	1346
Db	429	TTTTCAGTGTCTCTGTGGGAACTGTGTACACAGGAGGTATCCCTTTCTACCTCTCCAA	370
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QY	1407	TTTCCCTCATGTGTGTAACTCATGAAAGATCTGTATGATGATGATGATGATGATGATGATGATG	1465
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QY	1466	CCAAATTTGACATATTTGTGCTTATCTTTGAAAGATGACAGACCAATAGACCTGGAAGG	1525
Db	250	CCAAATTTGACATATTTGTGCTTATCTTTGAAAGATGACAGACCAATAGACCTGGAAGG	191
QY	1526	TCTTTGCTGAACTCCAGAGGTGTGGGACATGTTGGGGGAATGACCTTCCCAANGA	1585
Db	190	TCTTTGCTGAACTCCAGAGGTGTGGGACATGTTGGGGGAATGACCTTCCCAANGA	131

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1586 GCAGGCTCTGGTGGCTCCCGGCTCCAGTCAATGGTACTA--CCCGAGCTGGGGTCC 1643
130 GCAGGCTCTGGTGGCTCCCGGCTCCAGTCAATGGTACTA--CCCGAGCTGGGGTCC 71
1644 ATCCCTTCCCGGCTCCCGGCTCCAGTCAATGGTACTA--CCCGAGCTGGGGTCC 1701
70 ATCCCTTCCCGGCTCCCGGCTCCAGTCAATGGTACTA--CCCGAGCTGGGGTCC 11
1702 CTTGGCCACAT 1711
10 CTTGGCCACAT 1

RESULT 4
AL528727
LOCUS
DEFINITION
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  cDNA clone CS0DD001YK18 5-PRIME, mRNA sequence.
ACCESSION
  AL528727
VERSION
  AL528727.2 GI:31066577
KEYWORDS
  EST.
SOURCE
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  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
  Full-length cDNA libraries and normalization
  Unpublished
  On Feb 13, 2001 this sequence version replaced gi:12792220.
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  BP 191 91006 EVRY cedex - France
  Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
  Library was constructed by Life Technologies, a division of
  Invitrogen. This sequence belongs to sequence cluster 6100.f For
  more information about this cluster, see
  http://www.genoscope.cns.fr/
  cgi-bin/cluster.cgi?seq=CS0DD001BF09QPl&cluster=6100.f. Contact :
  Feng Liang, Email : fliang@lifetech.com URL :
  http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
  Faraday Avenue Genoscope sequence ID : CS0DD001BF09QPl.
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        /note="1st strand cDNA was primed with a NotI-oligo(dT)
        primer. Five prime end enriched, double-strand cDNA was
        digested with Not I and cloned into the Not I and EcoR V
        sites of the pCMVSPORT 6 vector. Library was normalized."
        BASE COUNT
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          Query Match 54.5%; Score 974.4; DB 9; Length 1201;
          Best Local Similarity 92.9%; Pred. No. 1.5e-137;
          Matches 1048; Conservative 17; Mismatches 49; Indels 14; Gaps 4;

661 TGGAGGGGACACCCCGGCTCCCGGCTCCAGTCAATGGTACTA--CCCGAGCTGGGGTCC 720
65 TGGAGGGGACACCCCGGCTCCCGGCTCCAGTCAATGGTACTA--CCCGAGCTGGGGTCC 124
721 GACTTCAACAGCTTAACTTCTGACGAGCTCAACGAGATCACTCTGGAGAGCTATGG 780
125 GACTTCAACAGCTTAACTTCTGACGAGCTCAACGAGATCACTCTGGAGAGCTATGG 184
781 AAGGCCCGCTGGCAGGGCAATGACATTGTCTGTAAGGCTGCTGAAGGTTTCGAGACTGGAGT 840
185 AAGGCCCGCTGGCAGGGCAATGACATTGTCTGTAAGGCTGCTGAAGGTTTCGAGACTGGAGT 244

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QY 841 ACAAGGAAGAGCAGGGACTTCAATGAAGAGTGTCCCGGCTCAGATTTTCTCGCATCA 900
DB 245 ACAAGGAAGAGCAGGGACTTCAATGAAGAGTGTCCCGGCTCAGATTTTCTCGCATCA 304
QY 901 AATGTGTCTCCAGTGTAGTGTGCTCCAGTGTCTCCAGTGTCTCTCTCTCTCTCTCTCT 960
DB 305 AATGTGTCTCCAGTGTAGTGTGCTCCAGTGTCTCCAGTGTCTCTCTCTCTCTCTCTCT 364
QY 961 ACACACTGGATGCGGTATGGATCCCTTACAAATGTACTACATGAAGGACCAATTTCTGTC 1020
DB 365 ACACACTGGATGCGGTATGGATCCCTTACAAATGTACTACATGAAGGACCAATTTCTGTC 424
QY 1021 GTGACACAGAGCCAGGCTGTGAAGTGTGTTTGACATGGCAAGGGGATGGCTTCTCTA 1080
DB 425 GTGACACAGAGCCAGGCTGTGAAGTGTGTTTGACATGGCAAGGGGATGGCTTCTCTA 484
QY 1081 CACACACTAGAGCCCTCATCTCCACGACATGCACTCAATAGCCGTAGTGTAAATGATGAT 1140
DB 485 CACACACTAGAGCCCTCATCTCCACGACATGCACTCAATAGCCGTAGTGTAAATGATGAT 544
QY 1141 GAGGACATGACTGCCGAAATTTAGCATGGCTGATGTCAGTTCCTTTTCCAATGCTCTGGT 1200
DB 545 GAGGACATGACTGCCGAAATTTAGCATGGCTGATGTCAGTTCCTTTTCCAATGCTCTGGT 604
QY 1201 CGCATGTATGACCTGCTGGGTAGCCCCGAACTCTGCAGAAAGAGCCCTGAAGACACA 1260
DB 605 CGCATGTATGACCTGCTGGGTAGCCCCGAACTCTGCAGAAAGAGCCCTGAAGACACA 664
QY 1261 AACAGAGCTCAGCAGACATGTGGAGTTTTCAGTGTCTTGTGGGAATCTGTGACACGG 1320
DB 665 AACAGAGCTCAGCAGACATGTGGAGTTTTCAGTGTCTTGTGGGAATCTGTGACACGG 724
QY 1321 GAGTACCTTTTGTGACCTTCCAAATATGAGATTTGGAATGGAATGGGATTTGGAAGGC 1380
DB 725 GAGTACCTTTTGTGACCTTCCAAATATGAGATTTGGAATGGAATGGGATTTGGAAGGC 784
QY 1381 CTTGGGCTACCATCCACAGGATTTTCCCTCATGTGTGTAAGCTCATGAAGATCTGC 1440
DB 785 CTTGGGCTACCATCCACAGGATTTTCCCTCATGTGTGTAAGCTCATGAAGATCTGC 844
QY 1441 ATGAATGAAGACCTGCAAGCGACCCAAATTTGACATGATTTGCTCTCTCTCTCTCTCT 1500
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QY 1501 ATGAGGACACATGAGGATGCAAGGCTCTTGGCTGAACTCCAGAGGTGTCTGGGACATGGT 1560
DB 905 ATGAGGACACATGAGGATGCAAGGCTCTTGGCTGAACTCCAGAGGTGTCTGGGACATGGT 964
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DB 965 TGGGGGGAATGCACCTCCCAAGAGCAGGCTCTTGGTTCCTCCCGGCTCCAGTCA 1024
QY 1620 TGGTACTACCCAGCCTGGGCTCCATCCCTTCCCTCCCTACCTACCTGTGCGCAAGAG 1679
DB 1025 TGGTACTACCCAGCCTGGGCTCCATCCCTTCCCTCCCTACCTACCTGTGCGCAAGAG 1082
QY 1680 GGGGGGCTCAGAGCTTTGTCATGTCACATGTCGTCTCCCAACATGGGAGGATCAGC 1739
DB 1083 GGGGGGCTCAGAGCTTTGTCATGTCACATGTCGTCTCCCAACATGGGAGGATC 1131
QY 1740 CCCGCTGTCTCAATAAAGTTTATATGAAAAAATAAAAAAAAAAAAAA 1787
DB 1132 ASCCGCTKTTAAATTAATTTWTGAAAAAATAAAAAAAAAAAAAA 1179

RESULT 5
AL579748
LOCUS
DEFINITION
  AL579748 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
  Homo sapiens cDNA clone CS0DU003YK18 5-PRIME, mRNA sequence.
ACCESSION
  AL579748
VERSION
  AL579748.2 GI:31318028

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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 16, 2001 this sequence version replaced gi:12945094.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Library: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Invitrogen. This sequence belongs to sequence cluster 6100.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D003BF09NP1&cluster=6100.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradey Avenue Genoscope sequence ID : CS0D003BF09NP1.
Location/Qualifiers
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/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 295 a 303 c 319 g 245 t 39 others
ORIGIN

Query Match 54.1%; Score 968.6; DB 9; Length 1201;
Best Local Similarity 98.4%; Pred. No. 1.1e-136;
Matches 1005; Conservative 4; Mismatches 8; Indels 4; Gaps 3;

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DB 82 TGGATCACTCCACAGTCTCTAGGCTTCCCAATCCAGGAGACTCGGCGCGGAGCGTG 141
QY 155 CTATGAGACGACATTTTCACTAGTGCAGGAGGAGGACGACGAGTGCCTGTGGC 214
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DB 332 TCAATGTAATGAACCGTGGGATGACACCCCTTGATCTGGCAGCACTGAGACACC 381
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DB 382 GTGATATTGTACAGAAGCTATTGCACTAAGGAGAGCACTCAATGAGATGAAACAG 441
QY 455 GGAATGTGCCCCGTGCACTATGCTGTTTGGGGCCAAGATCAAGTGCAGAGCACTGG 514

DB 442 GGAATGTGCCCCGTGCACTATGCTGTTTGGGGCCAAGATCAAGTGCAGAGCACTGG 501
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QY 575 CCAAGGACACCCCTGAGAGAGCTTCTCCAGAGCGGGCAGAGAAAGATGGGCCAGATTC 634
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DB 682 GAACCTTGAACAAACACTCTGTCATTTGACTTAAACACTTAACTTCTGTGACGAAGCTCA 741
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DB 922 CACGCTGCTCATCTCTACTCTCATCACACACTGATGCGGATGATGATCCCTCAATG 981
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DB 1039 A 1039

RESULT 6
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LOCUS AL528726 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
DEFINITION cDNA clone CS0D001YK18 3-PRIME, mRNA sequence.
ACCESSION AL528726
VERSION AL528726.2 GI:31066576
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 13, 2001 this sequence version replaced gi:12792219.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Library: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Invitrogen. This sequence belongs to sequence cluster 6100.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D001BF09NP1&cluster=6100.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradey Avenue Genoscope sequence ID : CS0D001BF09NP1.
Location/Qualifiers

FEATURES


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source
1. 1201
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/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      258 a      299 c      314 g      294 t      36 others
ORIGIN
Query Match      53.9%; Score 963.8; DB 9; Length 1201;
Best Local Similarity 95.5%; Pred. No. 5.8e-136;
Matches 1053; Conservative 11; Mismatches 30; Indels 9; Gaps 7;

QY 663 GAAGGGACACCCGACCTCGGCCCCGAAATGGAAACCTGGAACAACTCTGGCATTTGA 722
DB 1098 GGAAGGGACACCCGAACTCGCCCCGAAAT-GAACCTGHWACAAACACCTGGCATTTA 1040

QY 723 CTTCAACAGCTTAATCTCTGAGCAAGCTCAACGAGAAATC-ATCTGGAGAGTATGGA 781
DB 1039 CTYCACACCGCTTAATCTCCCTGACGAAGCTCMACGARAATMAACTCTGGAGAGCTATGGA 980

QY 782 AGGCCCGCTGCAGGGCAATGACATTGTCGTGAGGTGCTGAGGTTTCGAGACTGGAGTA 841
DB 979 A-GGCCGCTGGCAGGGCAATGAAATGTCGTGAGGTGCTGAGGTTTCGAAACTGGAGTA 921

QY 842 CAAGGAAGCAGGAGACTTCAATGAAGAGTGTCCCCGGCTCAGGATTTTCTCGCATCAA 901
DB 920 CAAGGGAGGAGGAGACTTCAATGAAGAGTGTCCCCGGCTCAGGATTTTCTCGCATCAA 861

QY 902 ATGTGCTCCCAGTGTAGGTGCTGCCAGTCTCCACCTGCTCCCTCATCTCTCATCA 961
DB 860 ATGTGCTCCCAGTGTAGGTGCTGCCAGTCTCCACCTGCTCCCTCATCACTCTCTCAA 801

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QY 1022 TGGACACAGCAGGCTGTGAAGTTTGTCTTGGACATGGCAGGGGCGATGCCCTTCCTAC 1081
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DB 680 ACACACTAGAGCCCTCTATCCACGACATGACACTCAATAGCCGTAGTGTAAATGATGATG 621

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QY 1202 GCATGTATGACCTGCTCCCTGAGTCCCGGAGCTCTGCAGAAAGGCTTGAAGACACAA 1261
DB 560 GCATGTATGACCTGCTCCCTGAGTCCCGGAGCTCTGCAGAAAGGCTTGAAGACACAA 501

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DB 500 ACAGACGCTCAGACAGATGAGAGTTTTCAGTGTCTTCTGTGGAACTGTGTACACGGG 441

QY 1322 AGGTACCTTTGCTGACCTCTCCAAATGAGATTGGAATGAGTGGCAATGGAAGGCC 1381
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DB 322 TGAATGAAGACCTCTGCAAAAGGACCCAAATTTTACATGATGTCGCTATCCTTGGGAGA 263

QY 1502 TGCAGGCAAGTAGGACTGGAAGGTCTTGCCTGAACTCCAGAGGTGTCCGGACATGTT 1561
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QY 1622 GTACTACCCAGCC-TGGGGTCCATCCCTTCCCTCCCTCCCTTCCCTTCCCTTCCCT 1678
DB 142 GTACTACCCAGCCATGGGTCCATCCCTTCCCTCCCTTCCCTTCCCTTCCCTTCCCT 83

QY 1679 GGGCGGGCTCCAGAGCTTTGTCACTTGCACATGCTGTCTCCCAACATGGGAGGATCAG 1738
DB 82 GGGCGGGCTCCAGAGCTTTGTCACTTGCACATGCTGTCTCCCAACATGGGAGG-TCAG 24

QY 1739 CCCCCTGTGCACAAATAAAGTTT 1761
DB 23 CCCCCTGTGCACAAATAAAGTTT 1

RESULT 7
AL528689
LOCUS
DEFINITION
AL528689 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
CDNA clone CS0DD001YE07 5-PRIME, mRNA sequence.
ACCESSION
AL528689
VERSION
AL528689.2 GI:31066539
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1201)
AUTHORS
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
COMMENT
On Feb 13, 2001 this sequence version replaced gi:12792182.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Library: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Email: segre@genoscope.cns.fr, a division of
Invitrogen. This sequence belongs to sequence cluster 6100.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DD001AC04QPI&cluster=6100.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0DD001AC04QPI.
FEATURES
Location/Qualifiers
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/clone="CS0DD001YE07"
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/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      287 a      314 c      332 g      250 t      18 others
ORIGIN
Query Match      53.3%; Score 952.8; DB 9; Length 1201;
Best Local Similarity 97.1%; Pred. No. 2.6e-134;
Matches 981; Conservative 9; Mismatches 16; Indels 4; Gaps 2;

QY 108 CAGTCTCAGGCTTCCCAATCCAGGGACATCGGGCGGGGACGCTGCTGAGGACGAT 167
DB 116 CCGTCTCAGGCTTCCCAATCCAGGGACATCGGGCGGGGACGCTGCTGAGGACGAT 175
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QY	1513	TAGAGCTGGAAGGTCCTTGCCGAACTCCAGAGGTGTGGGACATGTTGGGGGAATCA	1572
Db	212	TAGAGCTGAAGTCTCTTGCCGAACTCCAGAGGTGTGGGACATGTTGGGGGAATCA	153
QY	1573	CCTCCCAAGACGACGAGCCTCTGTGGTTCCTCCCGGCTCCAGTCATGTGTAACCCCA	1632
Db	152	CCTCCCAAGAGACGAGGCTCTGGTTCGCTCCCGCTCCAGTCATGTGTAACCCCA	93
QY	1633	GCC-TGGGGTCCATCCCTTTCCTCCCATCCCTACCACTGTG--CGCAAGAGGGGCGGGCTC	1688
Db	92	GCCATGGGGTCCATCCCTTCCCGGCTCCATCCCTACCACTGTGGGCCCAAGAGGGGCGGGCTC	33
QY	1690	AGAGCTTGTCACTGCGACATGGTGTCTCC	1121
Db	32	AGAGCTTGTCACTTGGCCACATGGTGTCTCC	1
RESULT 10			
AL569057/c			
LOCUS	AL569057	1201 bp	mRNA linear EST 13-MAY-2003
DEFINITION	AL569057 Homo sapiens PLACENTA	Homo sapiens cDNA clone CS0DE003D17	
	3-PRIME, mRNA sequence.		
ACCESSION	AL569057		
VERSION	AL569057.2	GI:30605114	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 1201)		
AUTHORS	Li W.B., Gruber C., Jessee J. and Polayes D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	unpublished		
COMMENT	On Feb 16, 2001 this sequence version replaced gi:12924017.		

Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: segr@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6100.f For
more information about this cluster, see
[http://www.genoscope.cns.fr/
cg3-bn/cluster.cgi?seq=CS0DE003CB09NP1&cluster=6100.f](http://www.genoscope.cns.fr/cg3-bn/cluster.cgi?seq=CS0DE003CB09NP1&cluster=6100.f). Contact :
Feng Liang Email : fliang@lifetech.com URL :
[http://fulllength.invitrogen.com/Invitrogen Corporation 1600](http://fulllength.invitrogen.com/Invitrogen_Corporation_1600)
Paradey Avenue Genoscope sequence ID : CS0DE003CB09NP1.
Location/Qualifiers
1..1201

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/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

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Query Match	52.3%	Score 935;	DB 9;	Length 1201;
Best Local Similarity	93.2%;	Pred. No. 1.3e-131;		
Matches 1007;	Conservative	20;	Mismatches 8;	Gaps 5;
QY	649	AAGGACATTTGGAGGGGACCCGGCACTGGCCCGGAATGAACTGAACCTGAACAA	708	
DB	1087	AAAAAGACAMATTTGGAGGGGCCACCCGGCACTCGCCCGGAATGAACCTTGACACAAMA	1028	
QY	709	CACCTGGCATTTGACCTTCAACAGCTTAACCTTCGACGAAAGCTCAAGAGATCACTCT	768	
DB	1028	TTCT---GCATTGACCTTCAMACAGTTAACTCCCTGAGAAAGCTACCGAAGAAATCACTCT	972	

QY	769	GGAGAGCTATGGAAGGGCCCTGGCAGGCGCAATGACATTGTCTGGAAGGTGCTGAAGTT	828
Db	971	GGAAAGCTATGGAAGGGCCCTGGCAGGCGCAATGACATTGTCTGGAAGGTGCTGAAGTT	912
QY	829	CGAGACTGAGGTAACAAGGAAGAGGAGGACTTCAATAAGAGTGTCCCGGCTCAGATT	888
Db	911	CGAATCTGAGMAACAAGGAAGAGGAGACTTCAATAAGAGTGTCCCGGCTCAGATT	852
QY	889	TTCTGCAATCCAAATGTGCTCCAGTGTAGTGTCTGCAAGTCTCCAGTCTCTCAT	948
Db	851	TTCTGCAATCCAAATGTGCTCCAGTGTAGTGTCTGCAAGTCTCCAGTCTCTCAT	792
QY	949	CCATCTCTCATACACACTGGAATGCGGTATGGAATCCCTCTACAAATGATCAATGAAGGC	1008
Db	791	CCATCTCTCATACACACTGGAATGCGGTATGGAATCCCTCTACAAATGATCAATGAAGGC	732
QY	1009	ACCAATTTTCGTGCGAGCACAGAGCCAGAGCTGTGAAGTTTCTTGGACATGCAAGGGGC	1068
Db	731	ACCAATTTTCGTGCGAGCACAGAGCCAGAGCTGTGAAGTTTCTTGGACATGCAAGGGGC	672
QY	1069	ATGGCCTTCTACACACACTAGAGCCCTCATCCACGACATGACTCAATAGCCGTAAT	1128
Db	671	ATGGCCTTCTCTACACACACTAGAGCCCTCATCCACGACATGACTCAATAGCCGTAAT	612
QY	1129	GTAATGATGATGAGGACATGACTGCGCCGAATTAGCATGCTGATGCAAGTTCTCTTC	1188
Db	611	GTAATGATGATGAGGACATGACTGCGCCGAATTAGCATGCTGATGCAAGTTCTCTTC	552
QY	1189	CAATGTCTCTGTCATGATGACACTGCTCGGTAGCCCCCGAAGCTCTGCAGAAAG	1248
Db	551	CAATGTCTCTGTCATGATGACACTGCTCGGTAGCCCCCGAAGCTCTGCAGAAAG	492
QY	1249	CCTGAAGACAAACAGACGCTCAGAGACATGTGAGGTTTTCAGAGTCTTCTGTGGAA	1308
Db	491	CCTGAAGACAAACAGACGCTCAGAGACATGTGAGGTTTTCAGAGTCTTCTGTGGAA	432
QY	1309	CTGTGTGACACGGGAGTACCTCTTGTGACCTCTCCAAATGAGATTGGAATGAAGTG	1368
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QY	1369	GCATTGGAAGGCTTTCGCTCAATCCATCCACAGGATATTTCCCTCATGTGTAGCTC	1428
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QY	1489	ATCCTTGGAAGATGATGAGCAAGATGAGACTGTGAAGTCTCTGCTGAACCTCCAGAGTG	1548
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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
ALU55417.2 GI:31277224			
994 bp mRNA linear EST 31-MAY-2003			
ALU55417 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens			
CDNA clone CS0DK008Y014 5-PRIME, mRNA sequence.			
ALU55417			

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KEYWORDS      EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE         1 (bases 1 to 994)
JOURNAL       Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
COMMENT       Full-length cDNA libraries and normalization
              Unpublished
              On Feb 15, 2001 this sequence version replaced gi:12897130.
              Contact: Genoscope
              Genoscope - Centre National de Sequencage
              BP 191 91006 EVRY cedex - France
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
              Library was constructed by Life Technologies, a division of
              Invitrogen. This sequence belongs to sequence cluster 6100.f For
              more information about this cluster, see
              http://www.genoscope.cns.fr/
              cgi-bin/cluster.cgi?seq=CS0DK008B070P1&cluster=6100.f. Contact :
              Feng Liang Email : fliang@lifetech.com URL :
              http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
              Faraday Avenue Genoscope sequence ID : CS0DK008B07QF1.
              Location/Qualifiers
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                /note="1st strand cDNA was primed with a NotI-oligo(dT)
                primer. Five prime end enriched, double-strand cDNA was
                digested with Not I and cloned into the Not I and EcoR V
                sites of the pCMVSPORT 6 vector. Library was normalized."
              244 a 265 c 282 g 199 t
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              Query Match 51.2%; Score 915.8; DB 9; Length 994;
              Best Local Similarity 98.4%; Pred. No. 1.1e-126;
              Matches 934; Conservative 1; Mismatches 13; Indels 1; Gaps 1;

QY 35 CCGGAGAGAGTCTCTGACGCCGAGTCCGAGGATAAAGCTTGGGGTTTCATCTCTCTCC 94
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QY 46 CCGGTCCGAATTCGCGGATCGAGTCCGAGGATAAAGCTTGGGGTTTCATCTCTCTCC 105
DB |||||
QY 95 CTGGATCACTCAGAGTCTCAGGCTTCCCAATCCAGGGACTCGGCGCGGGACGCTG 154
DB |||||
QY 106 CTGGATCACTCAGAGTCTCAGGCTTCCCAATCCAGGGACTCGGCGCGGGACGCTG 165
DB |||||
QY 155 CTATGGACGATTTTCACTCAGTCCGCGGAGGCAACGAGTCGCCGTTGCGCTGTGGC 214
DB |||||
QY 166 CTATGGACGATTTTCACTCAGTCCGCGGAGGCAACGAGTCGCCGTTGCGCTGTGGC 225
DB |||||
QY 215 TGGCAACACGAGAGACCTTCAACAGGGGAGCATGATGGCTTCTCCCTCTGCACT 274
DB |||||
QY 226 TGGCAACACGAGAGACCTTCAACAGGGGAGCATGATGGCTTCTCCCTCTGCACT 285
DB |||||
QY 275 GGGCTCCGAGAGGGCCGCTCTGCTGTGTTGAGATGTTGATCATGCGGGGGACCGA 334
DB |||||
QY 286 GGGCTCCGAGAGGGCCGCTCTGCTGTGTTGAGATGTTGATCATGCGGGGGACCGA 345
DB |||||
QY 335 TCAATGTAATGACCGTGGGATGACCCCTCTGATCTGGCAGCCAGTCATGACACC 394
DB |||||
QY 346 TCAATGTAATGACCGTGGGATGACCCCTCTGATCTGGCAGCCAGTCATGACACC 405
DB |||||
QY 395 GTGATATTGTACAGAGCTATTGCAAGTACAAGGAGACATCAATGCAGTGAATGAACAG 454
DB |||||
QY 406 GTGATATTGTACAGAGCTATTGCAAGTACAAGGAGACATCAATGCAGTGAATGAACAG 465
DB |||||
QY 455 GGAATGTGCCCTGCACTATGCTCTTTTGGGGCCAAAGATCAAGTGCAGAGACCTGG 514
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QY 466 GGAATGTGCCCTGCACTATGCTCTTTTGGGGCCAAAGATCAAGTGCAGAGACCTGG 525
DB |||||

QY 515 TGGCAATGGGGCCCTTGTGAGCATCTGTACAGATATGGAGATGCTCTGGACAAG 574
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QY 575 CCAAGGACCCCTCAGAGAGCTTCTCGAGAGCGGGCAGAGAAGATGGCCAGAAATCTCA 634
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DB |||||
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QY 886 CCGGCTCAGGATTTTCTCGCATCCAAATGTCTCCAGTCTAGGTGCTCCGCTGCGAGTCTC 945
DB |||||
QY 935 CACCT-GCTCTCATCTCTCTCTCTCATCACACATGGATGCGCTATGGAT 982
DB |||||
QY 946 CACCTGGCTCTCTCTCTCTCTCTCATCACACATGGATGCGCTATGGAT 994
DB |||||

RESULT 12
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LOCUS      AL514330 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
DEFINITION CLOBB011ZH02 5-PRIME, mRNA sequence.
ACCESSION  AL514330
VERSION     AL514330.2 GI:30464215
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1201)
AUTHORS     Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished
COMMENT     On Feb 13, 2001 this sequence version replaced gi:12777824.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 6100.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CLOBB011ZH02RPI&cluster=6100.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CLOBB011ZH02RPI.
            Location/Qualifiers
              1..1201
              /organism="Homo sapiens"
              /mol_type="mRNA"
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              /clone_lib="Homo sapiens NEUROBLASTOMA"
              /note="vector: pCMVSPORT 6; 1st strand cDNA was primed,
              with a NotI-oligo(dT) primer. Five prime end enriched,

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double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

BASE COUNT 289 a 288 c 309 g 251 t 64 others

Query Match 51.1%; Score 915; DB 9; Length 1201;
Best Local Similarity 94.7%; Pred. No. 1.3e-128;
Matches 944; Conservative 29; Mismatches 21; Indels 3; Gaps 3;

108 CAGTCTCAGGCTTCCCAATTCAGAGGAGCTGCGCGGAGCGCTGCTATGAGACAT 167
Db CCGTCTCAGGCTTCCCAATTCAGAGGAGCTGCGCGGAGCGCTGCTATGAGACAT 139

168 TTTCACTCAGTCCGCGGAGGCAACGAGTGGCGTTCGCTGCGGAGCAACAGCGA 227
Db TTTCACTCAGTCCGCGGAGGCAACGAGTGGCGTTCGCTGCGGAGCAACAGCGA 199

140 TTTCACTCAGTCCGCGGAGGCAACGAGTGGCGTTCGCTGCGGAGCAACAGCGA 199
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228 GAAAGACCTCAACAGAGGAGGAGATCATGGCTTCCCTTGCAGTGGGCTGCGGAG 287
Db GAAAGACCTCAACAGAGGAGGAGATCATGGCTTCCCTTGCAGTGGGCTGCGGAG 259

200 GAAAGACCTCAACAGAGGAGGAGATCATGGCTTCCCTTGCAGTGGGCTGCGGAG 259
Db GAAAGACCTCAACAGAGGAGGAGATCATGGCTTCCCTTGCAGTGGGCTGCGGAG 347

288 GGGCGGCTCTGCTGTGTTGAGATGTTGATCATGCGGGGCGACGATCAATGTAAG 347
Db GGGCGGCTCTGCTGTGTTGAGATGTTGATCATGCGGGGCGACGATCAATGTAAG 319

260 GGGCGGCTCTGCTGTGTTGAGATGTTGATCATGCGGGGCGACGATCAATGTAAG 319
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468 GCACTATGCTGTTTGGGCGCAAGATCAATGAGTGAATGAACAAGGGAATGTCCT 527
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LOCUS BX363152
DEFINITION BX363152 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
cDNA clone CS0DK009YD15 5-PRIME, mRNA sequence.
ACCESSION BX363152
VERSION BX363152.1 GI:30366685
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Li, W.B., Gruber, C., Jesses, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6100.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DK009CB08QPLcluster=6100.f. Contact :
Feng Liang Email : fliang@life.com URL :
http://fulllength.invitrogen.com/invitrogen Corporation 1600
Paradey Avenue Genoscope sequence ID : CS0DK009CB08QPL.

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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 286 a 305 c 318 g 244 t 48 others

Query Match 51.0%; Score 912.6; DB 13; Length 1201;
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141 ATTTCCTCAGTCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 200
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226 GAGAGACACCTCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 285
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201 GAGAGACACCTCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 260
Db GAGAGACACCTCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 345

286 GAGGCGGCTCTGCTGTGTTGAGATGTTGATCATGCGGGGAGGAGGAGGAGGAGGAG 345
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Db 501 GCCCTTGTGACATCTGTAAACAAGTATGAGAGATGCTGTGGCAACAAAGCCACGCC 560
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ACCESSION BX340064
VERSION BX340064.1 GI:30333861
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1201)
Li W.B., Gruber C., Jessee J. and Polayes D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
```

```
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6100.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1081CF01NP1&cluster=6100.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 264 a 281 c 305 g 305 t 46 others
ORIGIN
Query Match 51.0%; Score 911.6; DB 13; Length 1201;
Best Local Similarity 95.8%; Pred No. 4.2e-128;
Matches 976; Conservative 12; Mismatches 23; Indels 8; Gaps 5;
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QY	1560	TTGGGGGAATSCACCTCTCCCAAGCAGAGGCTTGTTGGTTCCTCCCGCTCTCAGTCA	1619
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ACCIONCTRN	U95400CC

ACCESSION	BX340065
VERSION	BX340065.1
KEYWORDS	GI:30335869
SOURCE	Est.
ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessen, J., and Polayars, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope

BP 191 91006 Evry cedex - France
Email: secre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6100.f For
more information about this cluster, see
[http://www.genoscope.cns.fr/
cg-bn/cluster.cgi?seq=CS0D1081Cf01P1c1cluster=6100.f](http://www.genoscope.cns.fr/cg-bn/cluster.cgi?seq=CS0D1081Cf01P1c1cluster=6100.f). Contact :
Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/>
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		/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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ORIGIN		

	Query Match	50.9%	Score 909.8	DB 13	Length 1201
Best Local Similarity	98.3%	Pred. No. 7,9e-128			
Matches 923	Conservative	6	Mismatches	8	Indels
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Db      125  TCCTCTCTTCCCTGGATCACTCCACAGTCTCTACGGCTTCCCCAAATCCAGGGGACTCGGGCG 184
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Db      245  CGCTGTGGCTGGACAACGAGAACGACTCAACACAGGGGGACGATCATGGCTTCTCC 304
OY      265  CCCTTGGACTGGGCGCTGCGAGAGGGCGGCTCTGCTGTGGTTGAGATGTTTGACATGGCGG 324
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OY      325  GGGGACCGGATCAATGTAATGAACCGTGGGGAGTGAACCCCGCTGCATCTGGCAGCAGT 384
Db      365  GGGGACCGGATCAATGTAATGAACCGTGGGGAGTGAACCCCGCTGCATCTGGCAGCAGT 424
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Db      425  CATGACACCGTGATATTGTACAGAACTATTGACATCAAGGCAGACATCAATGACGTG 484
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